

SEQUENCE LISTING

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<120> Mutagenesis of *Aspergillus* fungi and identification
 of genes essential for growth

<130> 346 723 - US

<150> PCT/IB 03/01 374

<151> 2003-03-13

<150> US 60/363 543

<151> 2002-03-13

<150> US 60/434 407

<151> 2002-12-19

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<170> PatentIn Ver. 3.2

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<213> *Aspergillus fumigatus*

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Gly Gly Ala Ala Pro Arg Gly Lys Ser Glu Leu Lys Ser Thr Asp Asp
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<213> *Aspergillus fumigatus*

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Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys
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Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser
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His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
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Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
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Asp	Glu	Val	Thr	Ser	Ser	Leu	Leu	Ser	Thr	Gly	Ser	Gly	Ser	Leu	Pro	165	170	175	
Lys	Ser	Pro	Ile	Leu	Ser	Ser	Ala	Cys	Pro	Gly	Trp	Ile	Cys	Tyr	Ala	180	185	190	
Glu	Lys	Thr	His	Pro	Phe	Ile	Leu	Pro	His	Leu	Ser	Arg	Leu	Lys	Ser	195	200	205	
Pro	Gln	Ala	Leu	Ser	Gly	Thr	Phe	Leu	Lys	Ser	Val	Leu	Ser	Lys	Ala	210	215	220	
Leu	Gly	Val	Pro	Pro	Ser	Gln	Ile	Trp	His	Leu	Ala	Ile	Met	Pro	Cys	225	230	235	240
Phe	Asp	Lys	Lys	Leu	Glu	Ala	Ser	Arg	Glu	Glu	Leu	Thr	Asp	Ile	Ala	245	250	255	
Trp	Ala	Ser	Thr	Phe	Thr	Gln	Ser	Gln	Thr	Thr	Pro	Val	Arg	Asp	Val	260	265	270	
Asp	Cys	Val	Ile	Thr	Thr	Arg	Glu	Leu	Leu	Thr	Leu	Ala	Thr	Ala	Arg	275	280	285	
Gly	Leu	Ser	Leu	Pro	Asn	Leu	Pro	Leu	Lys	Pro	Leu	Pro	Ala	Ser	Cys	290	295	300	
Leu	Thr	Pro	Phe	Pro	Asp	Gln	Ala	Leu	Glu	Ser	Phe	Leu	Phe	Ser	Lys	305	310	315	320
Ser	Ser	Ser	Gly	Gln	Thr	Val	Glu	Ser	Gly	Thr	Ser	Gly	Gly	Tyr	Leu	325	330	335	
His	His	Val	Leu	Gln	Ile	Phe	Gln	Ala	Arg	Asn	Pro	Gly	Ser	Lys	Ile	340	345	350	
Val	Thr	Gln	Arg	Gly	Arg	Asn	Ala	Asp	Val	Val	Glu	Tyr	Val	Leu	Met	355	360	365	
Ser	Ser	Gly	Asp	Glu	Pro	Leu	Phe	Arg	Ala	Ala	Arg	Tyr	Tyr	Gly	Phe	370	375	380	
Arg	Asn	Ile	Gln	Asn	Leu	Val	Arg	Lys	Leu	Lys	Pro	Ala	Arg	Val	Ser	385	390	395	400
Arg	Leu	Pro	Gly	Ala	Lys	Pro	Gln	Ala	Val	Ser	Ser	Ser	Ala	Asn	Arg	405	410	415	
Arg	Gln	Pro	Met	Ser	Arg	Asn	Ala	Ala	Pro	Ala	Gly	Thr	Gly	Ala	Asp	420	425	430	
Tyr	Ala	Tyr	Val	Glu	Val	Met	Ala	Cys	Pro	Gly	Gly	Cys	Thr	Asn	Gly	435	440	445	
Gly	Gly	Gln	Ile	Arg	Ile	Glu	Asp	Ala	Arg	Glu	Ala	Val	Pro	Asn	Ala	450	455	460	

Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
465 470 475 480

Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
485 490 495

Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser
500 505 510

Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
515 520 525

Glu Lys
530

<210> 7

<211> 942

<212> DNA

<213> *Aspergillus fumigatus*

<400> 7

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<210> 8

<211> 600

<212> DNA

<213> *Aspergillus fumigatus*

<400> 8

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acaactaaag aagatttcct ggatcttggt agcaagaatg cttttatcga gcatgcgcag 240
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aagatctgcg ttctcgacat tgagatgagg ggcgtgaaac aagtcaagcg caccgatctt 360
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gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgccaagc taaaaatgaa 480
ttggaatatg cggcgcagcc tggtctcat gataagattg tcgtgaacga tgacctggag 540
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<210> 9

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<400> 9

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Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
          35          40          45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
 50          55          60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
 65          70          75          80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
          85          90          95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Arg Gly Val
          100          105          110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
          115          120          125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
          130          135          140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
          145          150          155          160

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
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Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
          180          185          190

Gly Gly Asn Phe Gly Ala Arg Gln
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<210> 10

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<400> 10

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<210> 11

<211> 1923

<212> DNA

<213> *Aspergillus fumigatus*

<400> 11

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gcgaatcatt	tcgacgttgt	gttgattgat	actgccggtc	gccgtcataa	cgaccaacgc	1620
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<210> 12

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<400> 12

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Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
          35          40          45

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
          50          55          60

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser
          65          70          75          80

Leu Leu His Leu Gly Trp Ile Asp Lys Leu Leu Asp Asn Val Ser Thr
          85          90          95

Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg
          100          105          110

Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu
          115          120          125

Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu
          130          135          140

Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro
          145          150          155          160

Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu
          165          170          175

Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile
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Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser
          195          200          205

Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly
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Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val
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 Asn Ala Asp His Glu Lys Thr Lys Ser Ser Ser Thr Gly Phe Val
 305 310 315 320
 Gly Ser Gly Val Asn Ala Leu Gly Gly Phe Phe Arg Asn Ile Val Gly
 325 330 335
 Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met
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 Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg
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 Leu Cys Gln Gly Val Gln Arg Glu Leu Val Gly Lys Lys Thr Gly Asn
 370 375 380
 Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu
 385 390 395 400
 Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile
 405 410 415
 Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr
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 Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser
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 Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe
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 Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser

580	585	590
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His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr		
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Lys

<210> 13
 <211> 1564
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 13

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 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 15

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<400> 15

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      20              25              30

```

```

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
      35              40              45

```

```

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
      50              55              60

```

```

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
      65              70              75              80

```

```

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
      85              90              95

```

```

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
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```

```

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
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```

```

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
      130             135             140

```

```

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
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```

```

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
      165             170             175

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```

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu

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420						425						430					
Val	Ile	Ala	Gly	Phe	Leu	Val	Phe	Val	Val	Ala	Trp	Leu	Tyr	Ser	Ala		
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<210> 16

<211> 2376

<212> DNA

<213> Aspergillus fumigatus

<400> 16

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<210> 17

<211> 2145

<212> DNA

<213> *Aspergillus fumigatus*

<400> 17

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<210> 18

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<400> 18

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```

```

Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
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```

```

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
      50              55              60

```

```

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
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```

```

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
      85              90              95

```

```

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
      100             105             110

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```

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
      115             120             125

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```

Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
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```

```

Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg
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 180 185 190
 Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val
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 Val Thr Arg Phe Pro Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
 210 215 220
 Ala Lys Ala Ala Leu Leu Asn Asp Tyr Phe Ala His Glu Lys Tyr Asn
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 Gly Thr Leu Leu Val Arg Phe Asp Asp Thr Asn Pro Ser Asn Glu Lys
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 Gln Tyr Ala Leu Gln Ile Ile Lys Asp Gly Asn Ala Tyr Ala Asp Asp
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 305 310 315 320
 Lys Arg Arg Asp Ala Ser Val Glu Glu Asn Leu Ala Arg Phe Glu Glu
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 Met Lys Lys Gly Thr Pro Glu Gly Leu Arg Trp Cys Ile Arg Ala Lys
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 Tyr Pro Thr Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile Glu Gly
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 405 410 415
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 420 425 430
 Asp Phe Ala Arg Met Asn Phe Ile Arg Thr Leu Leu Ser Lys Arg Lys
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 450 455 460
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 465 470 475 480
 Ala Leu Arg Glu Phe Ile Leu Lys Gln Gly Pro Ser Lys Asn Ile Thr

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<210> 19

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<400> 19

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<210> 26

<211> 1479

<212> DNA

<213> *Aspergillus fumigatus*

<400> 26

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ccgtccttga cgatcaatta cgaggcaacg caggatcttg attctaccaa tgcttttgaa 120
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cagcccgccg gtctgaaggc tgttcggag gagatctgga aggacatgtt ggatctcgtc 240
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 300
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accgcccctt ctcgcggaat ctccgtcgcc gctgcgccct accgcgtctt ctacagccgc 480
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cggactatgg ataagctctt cctcaacggc agcgctaca tgattggcaa gatgaatggc 600
gagcactggg acttgtacct gactgaacct cataccatgc tcaccccgcc aacgagcccg 660
ggagccaaga ccgagtttac ggaaacggag accaagggtc tcagtgtacc ccagggcgct 720
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<210> 27

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<400> 27

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Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
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Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
      20             25             30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
      35             40             45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
      50             55             60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
      65             70             75             80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
      85             90             95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
      100            105            110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
      115            120            125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
      130            135            140

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Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
 145 150 155 160
 Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
 165 170 175
 Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
 180 185 190
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
 195 200 205
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
 210 215 220
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
 225 230 235 240
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
 245 250 255
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
 260 265 270
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
 275 280 285
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460

Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480

Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 28
 <211> 637
 <212> DNA
 <213> *Aspergillus fumigatus*

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 tccgccaaagg tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
 aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caaggtgggc 240
 aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctagattgct 300
 ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctcttc 360
 aagctgcagg aggaggagcg tgagcgcaag gatcagtaag ttcttgaggt ttccgctctg 420
 gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacaccaa ggaccttctc 480
 aagtccatgg gcgtaagtcc tgttctcaac gcggttggtc gtgggtttta agcagtcctg 540
 taacttatat tgcccactac agttcgacaa tctcaaggtc aacgttgtca acgtctcca 600
 acatcagggt caggagcgcc cccgccgctt ccggtag 637

<210> 29
 <211> 417
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 29
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 taccccaagt tgacgctcga ctttgagacc aacaagcgtc tttgcatga gatcgctatc 120
 attgcctcca agcgccttcg caacaagatt gctgggttaca ccaccacct tatgaagcgt 180
 atccagcgtg gccctgtccg cggatatctt ttcaagctgc aggaggagga gcgtgagcgc 240
 aaggatcagt acgttcctga ggtttcctgt ctggatgttt cccagaccga gtccggccag 300
 ctcgatgtcg atgccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
 gtcaacgttg tcaacgtctc ccaacatcag gttcaggagc gccccgcgg cttccgg 417

<210> 30
 <211> 139
 <212> PRT
 <213> *Aspergillus fumigatus*

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 Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
 20 25 30
 Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
 35 40 45
 Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
 50 55 60
 Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg

65		70		75		80
Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr						
	85			90		95
Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys						
	100			105		110
Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln						
	115			120		125
His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg						
	130			135		

<210> 31

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<400> 31

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gcaagaagg	tgtaagaag	aggaccgttg	atcctttctc	caggaaggac	gaatactctg	180
ttaaggtatg	tcgacgtgga	ctgtgtaagt	cgaccgcagc	taatctatat	caggcgcctt	240
ccactttcca	gatcagagag	tatgttgcac	gcatatgatg	tcgaatgcag	gataaaggcg	300
attcacaatg	gtagtggaga	ttatgctgac	tgaattatag	tgctcggaag	actctgggtca	360
accgcaccag	tggtctcaag	aacgcacaatg	actccctgaa	gggtcgaatt	ttcgaggtct	420
cgctggctga	cctgcagaat	gatgaagacc	atgctttccg	caaggttaag	cttcgtgtgg	480
acgaggttca	gggcaagaac	tgtttgacca	acttccacgg	tcttgatttc	acaaccgaca	540
aattgcgatac	cctcgtgcgc	aagtggcagt	cgctgatcga	agccatgtca	ctgtgaagac	600
gaccgatgat	tatctccttc	ggctttttgc	tatcgcttc	accaagagac	gcccgaacca	660
gattaagaag	accacatatg	ctcgttcttc	tcaaatacgt	gccatccgca	agaagatgat	720
tgaaatcatg	cagagggagg	cagccagctg	ctctctcgct	cagctcactc	acaagctcat	780
tcctgaggtc	attggctcgtg	agatcgagaa	ggctacccag	ggaatctatc	ctttgcagaa	840
tgtgtgtgac	cctgttatct	ttactcgagg	tgaagactaa	ctgcaatcta	ggtccatatt	900
cgcaaggtca	agcttcttaa	ggctcccaag	ttcgacctgg	gtgcactgct	gaatctgcac	960
ggtgaatcta	caaccgatga	taagggccac	aaggctcgaga	gagagttaa	ggagcagggt	1020
ctcgaaagcg	tttaa					1035

<210> 32

<211> 768

<212> DNA

<213> *Aspergillus fumigatus*

<400> 32

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agagatgtcg	ggaagactct	ggtcaaccgc	accagtggct	tcaagaacgc	caatgactcc	180
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ttccgcaagg	ttaagcttcg	tgtggacgag	gttcagggca	agaactgttt	gaccaacttc	300
cacggtcttg	atttcacaac	cgacaaattg	cgatccctcg	tgcgcaagtg	gcagtgcgtg	360
atcgaagcca	atgtcactgt	gaagacgacc	gatgattatc	tccttcggct	ttttgctatc	420
gccttcacca	agagacgccc	gaaccagatt	aagaagacca	catatgctcg	ttcttctcaa	480
atccgtgcca	tccgcaagaa	gatgattgaa	atcatgcaga	gggaggcagc	cagctgctct	540
ctcgctcagc	tcactcacia	gctcattcct	gaggtcattg	gtcgtgagat	cgagaaggct	600
accaggggaa	tctatccttt	gcagaatgtc	catattcgca	aggtcaagct	tcttaaggct	660
cccaagttcg	acctgggtgc	actgctgaat	ctgcacggtg	aatctacaac	cgatgataag	720
ggccacaagg	tcgagagaga	gttcaaggag	caggttctcg	aaagcggt		768

<210> 33

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<400> 33

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
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Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
          20           25           30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
          35           40           45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
          50           55           60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65           70           75           80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
          85           90           95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
          100          105          110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
          115          120          125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
          130          135          140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
          145          150          155          160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
          165          170          175

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
          180          185          190

Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
          195          200          205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
          210          215          220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
          225          230          235          240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
          245          250          255

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<210> 34
 <211> 614
 <212> DNA
 <213> *Aspergillus fumigatus*

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 cttctggcgg aacggtcctg tgttgggaaa ttgacggcta tcaatagcgc ctgctaaacg 180
 ggttatgtcc ctcaaagaac cgacgttgaa aatgtccaag tcccatgccg acagacgctc 240
 aaggatcatt cttacggatt cgcccgcaga aatctccaaa aagatcaatg ctgcgctcac 300
 agactcggaa ttaaccatta catatgaccc agtcgcgtcga cctggagtgg cgaatttaat 360
 agagatcttg agtcacttcg atggacgaac ttgcgatgag attgccatgg aataccgttc 420
 agccagtctt cgcgctctaa aggaacatct ggccagaacg ttgtccaatc atcttgagcc 480
 aataagagag aagtatctct cactttagg agatcagact gactaccttg attctatagc 540
 agaacagggt tctgaagccg cgcgggccaa cgctgaattg acaatggagc aagtcaaagt 600
 cgctatgggc ttaa 614

<210> 35
 <211> 552
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 35
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 aatcatgtat atggacccat tttcccgtca ccagaagcaa ttatatcgcc tgctaaacgg 120
 gttatgtccc tcaaagaacc gacgttgaaa atgtccaagt cccatgccga cagacgctca 180
 aggatcattc ttacggattc gcccgcgaga atctccaaaa agatcaatgc tgcgctcaca 240
 gactcggaa taaccattac atatgaccca gtccgtcgac ctggagtggc gaatttaata 300
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 gccagtcttc gcgctctaaa ggaacatctg gccagaacgt tgtccaatca tcttgagcca 420
 ataagagaga agtatctctc actttaggga gatcagactg actaccttga ttctatagca 480
 gaacagggtt ctgaagccgc gcggggccaac gctgaattga caatggagca agtcaaagtc 540
 gctatgggct ta 552

<210> 36
 <211> 184
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 36
 Pro Val Gly Asp Asp Gln Arg Gln His Leu Glu Phe Ser Arg Asn Thr
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 Ala Asn Ser Phe Asn His Val Tyr Gly Pro Ile Phe Pro Ser Pro Glu
 20 25 30
 Ala Ile Ile Ser Pro Ala Lys Arg Val Met Ser Leu Lys Glu Pro Thr
 35 40 45
 Leu Lys Met Ser Lys Ser His Ala Asp Arg Arg Ser Arg Ile Ile Leu
 50 55 60
 Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys Ile Asn Ala Ala Leu Thr
 65 70 75 80
 Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro Val Arg Arg Pro Gly Val
 85 90 95

Ala Asn Leu Ile Glu Ile Leu Ser His Phe Asp Gly Arg Thr Cys Asp
 100 105 110

Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser Leu Arg Ala Leu Lys Glu
 115 120 125

His Leu Ala Arg Thr Leu Ser Asn His Leu Glu Pro Ile Arg Glu Lys
 130 135 140

Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp Tyr Leu Asp Ser Ile Ala
 145 150 155 160

Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn Ala Glu Leu Thr Met Glu
 165 170 175

Gln Val Lys Val Ala Met Gly Leu
 180

<210> 37
 <211> 819
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 37
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 acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac 180
 gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct 240
 tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac 300
 acgatccgat catagcgtga agccctcatc tcccagctct cccgtctcct tgactccgaa 360
 gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcttc 420
 caggatcatc gccgcgaatt gcagcgcttg aacgccgcaa tcgccgagtc ccgcgaccga 480
 gccaatcttc tgtctaactg ccgctccgac attgatgcct accgcaattc aaaccccgcc 540
 gcggctgagg cagactacat gctcgaggag cggggtcgta tagatgaaag ccataacatg 600
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<210> 38
 <211> 681
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 38
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 ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag 180
 cgtgaagccc tcatctccca gctctcccg tctcttgact ccgaagccac tcttaccgca 240
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 aatcgccgta tcgtcgggtc tgccaataag gtaccaggaa tgaatgcatt gattggtaag 600
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<210> 39
 <211> 227
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 39
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 20 25 30
 Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
 35 40 45
 Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
 195 200 205
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe
 210 215 220
 Phe Phe Arg
 225

<210> 40
 <211> 1601
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 40
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aaggagattt cgtactcaca atgtaaaatc gtcggcaatg gatcgtttgg tgtcgtcttt 240
cagacgaaaa tgatgccaag cggcgaggat gctgccatta agagggtcct tcaagacaag 300
cgcttcaaag tatgtgtaca ttataagggc aattgccctc gctgccaac ccaaagatac 360
tgtcgtgac gagataccag aatcgagaac tgcagattat gcggattgtt cgccatccta 420
acatcgtaga attgaaagcc ttctattact cgaacggcga gagggtatgc gactctcctt 480
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cgcggtactt taataaaactc aaaacgacta tgccaatgtt ggaagtcaag ctgtatatct 660
atcaattgtt ccgttccctg gcatacatcc attcacaagg catctgccac cgtgacatca 720
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<210> 41

<211> 1182

<212> DNA

<213> *Aspergillus fumigatus*

<400> 41

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<210> 42

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<400> 42

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Lys	Thr	Thr	Met	Pro	Met	Leu	Glu	Val	Lys	Leu	Tyr	Ile	Tyr	Gln	Leu
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		210				215					220				
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Gly	Ile	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly	Thr	Pro	Thr
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Arg	Glu	Gln	Ile	Arg	Thr	Met	Asn	Pro	Asn	Tyr	Met	Glu	His	Lys	Phe
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Gln	Arg	Leu	Ser	Ala	Ile	Glu	Ala	Met	Cys	His	Pro	Phe	Phe	Asp	Glu
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 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg
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<210> 43

<211> 2209

<212> DNA

<213> *Aspergillus fumigatus*

<400> 43

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<210> 44
 <211> 2209
 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 45
 <211> 735
 <212> PRT
 <213> *Aspergillus fumigatus*

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 35 40 45

Phe Ile Lys Ser Met Trp Lys Ser Phe Lys Glu Lys His Ala Ser Lys
 50 55 60
 Phe Gly Gly Gly Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp
 65 70 75 80
 Leu Thr Thr Ile Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu
 85 90 95
 Val Ala Leu Ile Ala Gln Arg Met Arg Asp Gly Ile Glu Gln Asn Phe
 100 105 110
 Ser Asn Ala Pro Pro Ser Ser Gly Gln Ser Val Asn Tyr Glu Glu Lys
 115 120 125
 Arg Thr Gly Ser Leu Pro Gln Ser Thr Asp Ala Gln Glu Asp Gln Ser
 130 135 140
 Ser Ser Gly Ser Ala Ala Asn Gly Ser Arg Thr Asp Pro Gln Phe Lys
 145 150 155 160
 Asp Pro Glu Thr Ala Thr Cys Ala Leu Ser Lys Tyr Asp Asp Trp Arg
 165 170 175
 Asp Ser Val Leu Leu Arg Ile Gly Glu Val Val Asn Arg Asp Pro Glu
 180 185 190
 His Gly Glu Val Gln Ala Asn Glu Asn Pro Pro Ser Gly Gln Gln Ser
 195 200 205
 Gln Gln Ile Arg Ser Glu Glu Asp Asp Arg Ser Ile Arg Lys Leu Arg
 210 215 220
 Glu Val Phe Pro Pro Val Glu Thr Ser Leu Ser Gln Leu Pro Glu Ala
 225 230 235 240
 Lys Lys Leu Leu Ile Leu His Ser Leu Leu Leu Leu Val Leu Ser Leu
 245 250 255
 Glu His Tyr Asn Ala Trp Ser Arg Val Leu Met Leu Phe Val Thr Ser
 260 265 270
 Ser Leu Gly Leu Asp Val Lys Leu Leu Asn Glu Asp Glu Val Lys Val
 275 280 285
 Ala Arg Gly Leu Leu Asp Thr Ala Leu Ala Leu Ser Ser Asn Ala Pro
 290 295 300
 Arg Gln Asp Glu Ser Arg Ser Arg Asp Ser Ser Arg Lys Trp Lys Val
 305 310 315 320
 Gly Ile Ala Ser Val Ala Gly Ala Ala Leu Ile Gly Ile Thr Gly Gly
 325 330 335
 Leu Ala Ala Pro Leu Val Ala Ala Gly Leu Gly Thr Val Met Gly Gly
 340 345 350
 Leu Gly Leu Gly Ala Thr Ala Ala Ala Gly Tyr Leu Gly Ala Leu Ala
 355 360 365
 Gly Ser Gly Val Val Val Gly Gly Leu Phe Gly Ala Tyr Gly Gly Arg

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Ala	Phe	Leu	Pro	Ile	Arg	Gly	Ser	Arg	His	Arg	Ser	Glu	Asp	Glu	Arg
				405					410					415	
Glu	Ala	Ala	His	Gln	Asp	His	Arg	Leu	Arg	Val	Thr	Ile	Gly	Val	Thr
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Gly	Trp	Leu	Thr	Glu	Glu	Asp	Asn	Phe	Val	Ile	Pro	Trp	Arg	Val	Ile
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Gly	Ala	Glu	Ser	Glu	Val	Phe	Gly	Leu	Arg	Trp	Glu	Thr	Glu	Pro	Leu
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Thr	Ala	Gly	Glu	Gln	Val	Leu	Lys	Lys	Thr	Phe	Leu	Ser	Gln	Leu	Leu
				485					490					495	
Thr	Ala	Val	Ala	Leu	Pro	Leu	Gly	Leu	Leu	Lys	Val	Ala	Arg	Val	Val
			500					505					510		
Asp	Asn	Pro	Phe	Ser	Val	Ala	Lys	Ala	Arg	Ala	Asp	Lys	Ala	Gly	Glu
		515					520					525			
Val	Leu	Ala	Asp	Ala	Leu	Ile	Ser	Lys	Val	Gln	Gly	Glu	Arg	Pro	Val
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Thr	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Ser	Arg	Val	Ile	Phe	Ala	Cys	Leu
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Gln	Ser	Leu	Ala	Lys	Arg	Arg	Ala	Phe	Gly	Leu	Val	Glu	Ser	Ala	Ile
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		595					600					605			
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Arg	Ile	Leu	Ser	Val	Val	Gly	Leu	Glu	Ser	Ile	Asp	Ala	Arg	Glu	Val
			660					665					670		
Ala	Leu	Glu	Glu	Ala	Ala	Leu	Glu	Ala	Lys	Asp	Arg	Arg	Gln	Glu	Gln
		675					680						685		
Glu	Arg	Ala	His	Asn	Glu	Arg	Gln	Ala	Gly	Phe	Met	Gly	Glu	Gly	Arg
		690				695					700				

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Asp Arg Leu Gln Lys Glu Met Gly Lys Ala Arg Val Arg His Ser
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<210> 46

<211> 510

<212> DNA

<213> *Aspergillus fumigatus*

<400> 46

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<210> 47

<211> 423

<212> DNA

<213> *Aspergillus fumigatus*

<400> 47

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<210> 48

<211> 141

<212> PRT

<213> *Aspergillus fumigatus*

<400> 48

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20 25 30

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35 40 45

Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
50 55 60

His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala

65	70	75	80
Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly			
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Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg			
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Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys			
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<210> 49
 <211> 1413
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 49

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<210> 50
 <211> 1284
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 50

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ttatttgccg	atggcgatct	gattcctctc	ggacgacttc	aatcatacct	cggccctctc	300
atcgctaagc	gcagaacccc	aaagatccaa	cggcaatact	cggatatttg	tggaggggtca	360
ccgatcagga	aatgggtccga	gtatcagtg	gaggaaatgt	gcagattgct	agacaaaatc	420


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gtcgcgttca cacagtaccc ccaatattcg tgctccacca cgggtagctc gctgaacgag 600
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<210> 51

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<400> 51

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      20             25             30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
      35             40             45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
      50             55             60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
      65             70             75             80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
      85             90             95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
      100            105            110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
      115            120            125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
      130            135            140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
      145            150            155            160

Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
      165            170            175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
      180            185            190

Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
      195            200            205

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Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
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 Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
 225 230 235 240
 Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
 245 250 255
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
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 Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
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<210> 52

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 52

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<210> 53

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 53

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caaaagacct atttttctgc caatcggacc gcagatggct tacttgcatc cttatccgcc 240
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gagtcgatta cttcacagtc tacttcacaa gagttacctc atcgccggag gaagcggtta 360
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accctctcga cctcaacctt gacctttctc tacctgacca caggaacctt cttgtcttca 660
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attgcgactg ctgctgcagg tctcggtttg ttatacattg gaacgaaccc tacgactact 840
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<210> 54

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<400> 54

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 Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
 35 40 45
 Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr
 50 55 60
 Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala
 65 70 75 80
 Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly
 85 90 95
 Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu
 100 105 110
 Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn
 115 120 125
 Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr
 130 135 140
 Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala
 145 150 155 160
 Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr
 165 170 175
 Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu
 180 185 190
 Asp Pro Ser Met Thr Pro Leu Pro Thr Leu Ser Thr Ser Thr Leu Thr
 195 200 205
 Phe Leu Tyr Leu Thr Thr Gly Thr Phe Leu Ser Ser Cys Ser Ala Asn
 210 215 220
 Thr Leu Asn Met Leu Leu Glu Pro Lys Tyr Asp Ala Leu Met Ser Arg
 225 230 235 240
 Thr Arg Asn Arg Pro Leu Val Arg Gly Leu Leu Ser Arg Arg Ala Ala
 245 250 255
 Val Leu Phe Ala Ile Ala Thr Ala Ala Ala Gly Leu Gly Leu Leu Tyr
 260 265 270
 Ile Gly Thr Asn Pro Thr Thr Thr Ala Leu Ser Ala Ser Asn Ile Cys
 275 280 285
 Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Arg Ile Ser Val Ile Asn
 290 295 300
 Thr Trp Val Gly Ala Val Val Gly Gly Ile Pro Pro Leu Met Gly Trp
 305 310 315 320
 Thr Ala Ala Ala Gly Gln Thr Ala Thr Thr Gly His Asp Ser Trp Arg
 325 330 335
 Asp Met Leu Phe Ser Lys Asp Ser Ile Gly Gly Trp Leu Leu Gly Gly

340	345	350
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355	360	365
Ile Arg Glu Glu Tyr Lys Ala Ala Gly Tyr Arg Met Leu Ala Trp Thr		
370	375	380
Asn Pro Ala Ala Asn Ala Arg Val Ala Leu Arg Tyr Ser Leu Leu Met		
385	390	395
Phe Pro Phe Ser Val Gly Leu Trp Trp Val Gly Val Val Gly Asn Gly		
405	410	415
Phe Leu Val Gly Ser Thr Ala Ala Asn Gly Trp Leu Val Lys Glu Ala		
420	425	430
Tyr Lys Phe Trp Arg His Gln Gly Ala Asn Gly Ser Ala Arg Arg Leu		
435	440	445
Phe Trp Ala Ser Ile Trp Gln Leu Pro Ile Leu Leu Val Gly Gly Leu		
450	455	460
Val Thr Lys Lys Gly Leu Trp Asp Gly Val Trp Asn Asn Val Phe Gly		
465	470	475
Gln Pro Val Glu Asp Glu Asp Asp Tyr Leu Trp Glu Asp Glu Asp Glu		
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<210> 55

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 55

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1626

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<210> 56

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 56

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1626

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<210> 57

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<400> 57

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Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro
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Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser

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65					70					75					
Val	Ile	Asn	His	Asp	Cys	Pro	Ala	Glu	Thr	Pro	Pro	Pro	Ile	Leu	Pro
85					90					95					
Leu	Glu	Asn	Arg	Ala	Gly	His	Asp	Gln	Ser	Ser	Gln	Lys	Ala	Ser	Ser
100					105					110					
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115					120					125					
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130					135					140					
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145					150					155					
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195					200					205					
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210					215					220					
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225					230					235					
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245					250					255					
Arg	Asp	Val	Arg	Lys	Pro	Ser	Ala	Thr	Arg	Pro	Lys	Val	Leu	Gln	Thr
260					265					270					
Tyr	Lys	Lys	Leu	Leu	His	Glu	Val	Gly	His	Ala	Leu	Gln	Gln	Ser	Pro
275					280					285					
Ser	Phe	Ala	Glu	Arg	Val	Arg	Ile	Ile	Gly	Ser	Arg	Phe	Pro	Val	Leu
290					295					300					
Ser	Ala	Ile	His	Arg	Pro	Thr	Gly	Arg	Leu	Leu	Gln	Phe	His	Cys	Gly
305					310					315					
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325					330					335					
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 Gln Arg Pro Asp Cys Leu Gly Glu Gln Leu Ile Ala Phe Leu Arg Ala
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 Tyr Gly Ser Asp Ile Asp Leu Thr Thr Thr Gly Val Ser Val Asp Pro
 405 410 415
 Pro Ser Trp Phe Asn Ala Ser Thr Val Lys Arg Ala Ser Ala Leu Tyr
 420 425 430
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 Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His
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<211> 2356

<212> DNA

<213> *Aspergillus fumigatus*

<400> 58

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<213> *Aspergillus fumigatus*

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<213> *Aspergillus fumigatus*

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Leu Glu Ser Gly Leu Gly Arg Arg Asn Phe Val Pro Pro Arg Gln Val
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Pro Val Val Asp Ala Met Glu Arg Thr Lys Asn Ala Ile Gln Ser Asn
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Asn Ser Ser Ser Arg Ala Gln Leu Ser Asp Ala Leu Pro Glu Ser Glu
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Lys Ser Gln Ser Ala Gly Gln Val Ile Val Pro Thr Arg Met Gln Glu
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Leu Leu Asp Arg Gly Arg Pro Ile Glu Ala Ala Gln Phe Phe Leu Glu
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Thr His Ala Ala Ser Leu Lys Gly Ile Ser Ser Asp Arg Lys Glu Met
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Pro Pro Glu Met Val Asp Val Val Leu Arg Ser Leu Leu Glu Ser His
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Arg Leu Thr Thr Ala Lys Trp Phe Leu Leu Arg Asn Leu Gln His Asp
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Arg Asp Cys Gly Leu Cys Gly Ala Tyr Leu Ser Gly Leu Trp Arg Lys
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 Gly Val Asp Ala Gly Leu Gln Glu Met His Lys Leu Lys Leu Thr Arg
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 485 490 495
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<213> *Aspergillus fumigatus*

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<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296

Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 92
<211> 2052
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
      Genomic sequence containing the coding region

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<210> 93
<211> 2052
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
      Coding region without exons

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<400> 93

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<210> 94

<211> 683

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Protein sequence

<400> 94

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Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu Val Ala Leu Ile
35           40           45

Ala Gln Arg Met Arg Asp Gly Ile Glu Gln Asn Phe Ser Asn Ala Pro
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 100 105 110
 Ala Thr Cys Ala Leu Ser Lys Tyr Asp Asp Trp Arg Asp Ser Val Leu
 115 120 125
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 130 135 140
 Gln Ala Asn Glu Asn Pro Pro Ser Gly Gln Gln Ser Gln Gln Ile Arg
 145 150 155 160
 Ser Glu Glu Asp Asp Arg Ser Ile Arg Lys Leu Arg Glu Val Phe Pro
 165 170 175
 Pro Val Glu Thr Ser Leu Ser Gln Leu Pro Glu Ala Lys Lys Leu Leu
 180 185 190
 Ile Leu His Ser Leu Leu Leu Leu Val Leu Ser Leu Glu His Tyr Asn
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 290 295 300
 Ala Thr Ala Ala Ala Gly Tyr Leu Gly Ala Leu Ala Gly Ser Gly Val
 305 310 315 320
 Val Val Gly Gly Leu Phe Gly Ala Tyr Gly Gly Arg Met Thr Gly Arg
 325 330 335
 Met Val Asp Lys Tyr Ala Arg Glu Val Asp Asp Phe Ala Phe Leu Pro
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 370 375 380
 Glu Glu Asp Asn Phe Val Ile Pro Trp Arg Val Ile Gly Ala Glu Ser

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Gln Val Leu Lys Lys Thr Phe	Leu Ser Gln Leu Leu Thr	Ala Val Ala				
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Leu Pro Leu Gly Leu Leu Lys	Val Ala Arg Val Val Asp Asn Pro Phe					
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Ser Val Ala Lys Ala Arg Ala Asp Lys Ala Gly Glu Val Leu Ala Asp						
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Tyr Ser Leu Gly Ser Arg Val Ile Phe Ala Cys Leu Gln Ser Leu Ala						
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Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile Leu Met Gly Ala						
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Pro Thr Pro Ser Asn Ser Glu Gln Trp Cys Arg Ile Arg Ser Val Val						
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<210> 95

<211> 3814

<212> DNA

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 95

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<210> 96

<211> 2814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
Genomic sequence containing the coding region

<400> 96

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<210> 97

<211> 2814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
Coding region without exons

<400> 97

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<210> 98

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<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
Protein sequence

<400> 98

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Ala Pro Asn Tyr Asp Ala Thr Ser Ala Ala Lys Arg Leu Ala Arg Met
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Met Glu Ala Ala Glu Ala Gly Glu Phe Met Gly Leu Ala Ser Leu Lys
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Val Val Ala Leu His Gln Glu Gly Gly Phe Arg Arg Pro Gly Met Gly
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Thr Arg Ser Gln Leu Val Asp Ala Leu Ile Ser Arg Pro Asn Leu Glu
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Ser Gly Leu Gly Arg Arg Asn Phe Val Pro Pro Arg Gln Val Pro Val
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Val Asp Ala Met Glu Arg Thr Lys Asn Ala Ile Gln Ser Asn Asn Ser
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Trp Lys Thr Leu Met Leu Ala Leu Ala Lys Lys Gly Cys Ile Glu Ser						
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Val Ala Ser Val Tyr Thr Arg Tyr Met Arg Lys Phe Pro Cys Pro Pro						
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Pro Lys Phe Glu Lys Gln Pro Ser Asp Lys Leu Phe Asn Pro Val Ile						
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Asp Ala Gly Leu Gln Glu Met His Lys Leu Lys Leu Thr Arg Arg Arg						
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Ser His Ser Gly Ile Glu Ile Arg Asn Phe Val Phe Arg Tyr Leu Asp						
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Pro Leu Asp Ala Ser Arg Leu Phe Asn Gln Ser Asp Val Arg Glu Thr
885 890 895

Val Lys Arg Trp Asp Glu Glu Tyr Glu Leu Glu Ala Val Leu Gly Arg
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<210> 99

<211> 2401

<212> DNA

<213> Aspergillus fumigatus

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<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Genomic sequence containing 3' and 5'-ends and the coding region

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<220>
<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
      Genomic sequence containing the coding region

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<210> 101
<211> 1200
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
      Coding region without exons

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gccgaactat ttgtgatttt gtgcacaata gcctctatgg gatattcttc ccgaatgaca 480
cagtgaaga aggaacagct agctgacgtc ggccagagca aactccagtt gcctgataac 540
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<210> 102

<211> 399

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Protein sequence

<400> 102

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35        40        45

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50        55        60

His Leu Gly Asn Tyr Leu Gly Ala Leu Arg Glu Trp Val Arg Leu Gln
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Asn Ala Ala Lys Glu Gly Thr Arg Leu Phe Phe Ser Ile Val Asp Leu
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His Ala Leu Thr Val Pro Gln Asp Ala Ser Gln Leu Arg Asn Trp Arg
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Lys Glu Thr Phe Ala Thr Leu Ile Ala Val Gly Leu Asp Pro Asn Arg
115       120       125

Ser Thr Ile Phe Tyr Gln Ser Ala Val His Ala His Ala Glu Leu Phe
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Trp Ile Leu Cys Thr Ile Ala Ser Met Gly Tyr Leu Ser Arg Met Thr
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Gln Trp Lys Lys Glu Gln Leu Ala Asp Val Gly Gln Ser Lys Leu Gln
165       170       175

Leu Pro Asp Asn Ala Asn Leu Glu Asp Ser Thr Ala Arg Ser Arg Leu
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 Asp Gly Arg Thr Cys Asp Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser
 325 330 335
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<210> 103

<211> 3805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
 Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 104

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
 Genomic sequence containing the coding region

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<210> 105

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Coding region without exons

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gaagtacact	tctcgtcata	ttcaaaatca	aaggacaaca	aggcgaagaa	agcgagcgcg	2160
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ccacgtggca	agagcgagct	gaagagtagc	gacgatatcc	ggattgcgcg	caaattgaag	2760
cagaagagac	gagagaagaa	tgctcgtccc	tcgaggaaga	agtaa		2805

<210> 106

<211> 934

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Protein sequence

<400> 106

Met Pro His Arg Ala Ala Ser Pro Ala Val Ser Glu Asn Glu Phe Asp

1	5	10	15
Ile Thr Gly Ala Leu Phe Gln Asn Asp Ser Asp Ser Asp Asn Glu Gln	20	25	30
Pro Ser Ala Lys Ser Lys Arg Gln Pro Pro Lys Lys Val Pro Ser Gln	35	40	45
Ala Leu Asp Phe Leu Gly Asp Val Asn Glu Asp Asp Asn Asp Asp Glu	50	55	60
Ala Phe Ile Ala Glu Gln Gln Thr Ser Ala Asn Arg Lys Ala Ser Asn	65	70	75
Leu Lys Gly Arg Thr Val Lys Lys Gly Gly Gly Phe Gln Ala Met Gly	85	90	95
Leu Ser Ala Asn Leu Leu Lys Ala Ile Ala Arg Lys Gly Phe Ser Val	100	105	110
Pro Thr Pro Ile Gln Arg Lys Thr Ile Pro Val Ile Met Asp Asp Gln	115	120	125
Asp Val Val Gly Met Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Phe	130	135	140
Val Ile Pro Met Ile Glu Lys Leu Lys Ser His Ser Thr Lys Val Gly	145	150	155
Ala Arg Gly Leu Val Leu Ser Pro Ser Arg Glu Leu Ala Leu Gln Thr	165	170	175
Leu Lys Val Val Lys Glu Leu Gly Arg Gly Thr Asp Leu Lys Ser Val	180	185	190
Leu Leu Val Gly Gly Asp Ser Leu Glu Glu Gln Phe Ala Met Ile Ala	195	200	205
Gly Asn Pro Asp Ile Ile Ile Ala Thr Pro Gly Arg Phe Leu His Leu	210	215	220
Lys Val Glu Met Asn Leu Asp Leu Ser Ser Ile Arg Tyr Val Val Phe	225	230	235
Asp Glu Ala Asp Arg Leu Phe Glu Met Gly Phe Ala Ala Gln Leu Thr	245	250	255
Glu Ile Leu His Gly Leu Pro Ala Asn Arg Gln Thr Leu Leu Phe Ser	260	265	270
Ala Thr Leu Pro Lys Ser Leu Val Glu Phe Ala Arg Ala Gly Leu Gln	275	280	285
Glu Pro Thr Leu Val Arg Leu Asp Thr Glu Ser Lys Ile Ser Pro Asp	290	295	300
Leu Gln Asn Ala Phe Phe Ser Val Lys Ser Ser Glu Lys Glu Gly Ala	305	310	315
Leu Leu Tyr Ile Leu His Glu Val Ile Lys Met Pro Thr Gly Pro Thr	325	330	335

Glu Val Ser Gln Gln Arg Lys Glu Glu Asp Ala Ser Ala Lys Asn Leu
 340 345 350
 Lys Asn Lys Lys Arg Lys Arg Ala Glu Met Glu Lys Ala Val Asn Thr
 355 360 365
 Arg Glu Ser Pro Thr Lys His Ser Thr Ile Val Phe Ala Ala Thr Lys
 370 375 380
 His His Val Asp Tyr Leu Tyr Ser Leu Leu Cys Glu Ala Gly Phe Ala
 385 390 395 400
 Val Ser Tyr Val Tyr Gly Ser Leu Asp Gln Thr Ala Arg Lys Ile Gln
 405 410 415
 Val Gln Asn Phe Arg Thr Gly Met Thr Asn Ile Leu Val Val Thr Asp
 420 425 430
 Val Ala Ala Arg Gly Ile Asp Ile Pro Ile Leu Ala Asn Val Ile Asn
 435 440 445
 Tyr Asp Phe Pro Ser Gln Pro Lys Ile Phe Val His Arg Val Gly Arg
 450 455 460
 Thr Ala Arg Ala Gly Arg Lys Gly Trp Ser Tyr Ser Leu Val Arg Asp
 465 470 475 480
 Ala Asp Ala Pro Tyr Leu Leu Asp Leu Gln Leu Phe Leu Gly Arg Arg
 485 490 495
 Leu Val Val Gly Arg Glu Phe Gly Asp Gln Val Asn Phe Ala Glu Asp
 500 505 510
 Val Val Thr Gly Ser Leu Pro Arg Asp Gly Leu Ser Gln Ser Cys Glu
 515 520 525
 Trp Val Thr Lys Val Leu Asp Asp Asn Ala Asp Leu Ala Ala Gln Arg
 530 535 540
 Thr Val Ala Ala Lys Gly Glu Lys Leu Tyr Met Arg Thr Arg Asn Ala
 545 550 555 560
 Ala Ser Leu Glu Ser Ala Lys Arg Ser Lys Gln Val Val Ser Ser Asp
 565 570 575
 Asn Trp Thr Ser Val His Pro Leu Phe Gln Asp Glu Thr Ser Asn Leu
 580 585 590
 Glu Ala Glu Arg Glu Lys Met Leu Ala Arg Ile Gly Gly Tyr Arg Pro
 595 600 605
 Pro Glu Thr Ile Phe Glu Val Asn Asn Arg Arg Met Gly Lys His Glu
 610 615 620
 Asn Val Asp Ala Leu Asp Thr Ile Lys Arg Val Arg Ser Thr Leu Glu
 625 630 635 640
 Ser Lys Lys Lys Arg Ala Gln Ala Asn Glu Lys Ser Glu Phe Leu Glu
 645 650 655

Asp Gly Pro Asp Asp Gly Lys Ala Val Asn Glu Ala Lys Glu Thr Glu
 660 665 670
 Ser Glu Gly Ala Phe Ser Asp Glu Asp Asp Asp Val Pro Thr Gly Val
 675 680 685
 Ala Asp Asn Met Ser Met Ala Ser Asp Ser Glu Leu Glu Val Thr Phe
 690 695 700
 Ser Ser Tyr Ser Lys Ser Lys Asp Asn Lys Ala Lys Lys Ala Ser Ala
 705 710 715 720
 Ala Ser Phe Gln Asn Pro Glu Tyr Phe Met Ser Tyr Thr Pro Asn Asn
 725 730 735
 Thr Ser Leu Ala Glu Asp Arg Ala Tyr Gly Val His Ser Gly Thr Asn
 740 745 750
 Ser Asn Phe Ala Gln Ala Ser Arg Ser Ala Thr Met Asp Leu Ala Gly
 755 760 765
 Asp Asp Gly Gly Arg Gly Phe Gly Glu Ala Arg Thr Leu Met Arg Trp
 770 775 780
 Asp Lys Arg His Lys Lys Tyr Val Ala Arg Gln Asn Asp Glu Asp Gly
 785 790 795 800
 Ser Lys Gly Thr Arg Leu Val Arg Gly Glu Ser Gly Ala Lys Ile Ala
 805 810 815
 Ala Ser Phe Arg Ser Gly Arg Phe Asp Ala Trp Lys Arg Glu Asn Arg
 820 825 830
 Leu Gly Arg Leu Pro Arg Val Gly Glu Ala Glu Ala Ala Asn Leu Ala
 835 840 845
 Ala Gly Leu Asn Ala Ala Ile Ser Gly Lys Arg Phe Arg His Arg Lys
 850 855 860
 Glu Gln Ala Pro Lys Lys Ala Asp Pro Leu Arg Gly Asp Tyr Glu Lys
 865 870 875 880
 Met Lys Lys Lys Ala Glu Leu Ala Lys Glu Arg Ala Met Ser Lys Ala
 885 890 895
 Gly Gly Ala Ala Pro Arg Gly Lys Ser Glu Leu Lys Ser Thr Asp Asp
 900 905 910
 Ile Arg Ile Ala Arg Lys Leu Lys Gln Lys Arg Arg Glu Lys Asn Ala
 915 920 925
 Arg Pro Ser Arg Lys Lys
 930

<210> 107

<211> 2413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 107

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gcaagaagat	atggtcggta	tttacatcac	ctccttctct	gccttgagtg	cctaccgctc	180
tgctgcctgc	gtgcccaccg	acttcaccag	tgacgcgata	tcgtcatcgg	agcaacgcgg	240
gggaaacacg	aacatcacgt	gaatgcgcca	agacttgatg	accccaaatt	attactgatt	300
ggtcaaactt	ccagcactgt	tccgtcatca	accacctaag	ggcctagata	tggtctccag	360
ttacagatcc	ttcgtgccac	gattctttca	ttgagtggtc	aaatactact	cgacgtattt	420
ttgtgggctt	cagtttgtgg	ctaattgttag	accgatagac	gacggccaac	ctttttaata	480
cactatcacc	gcacctcccc	atggctctcc	gccggccatt	aacacttccg	aggcacattc	540
tcaatggagc	ttgttttaggc	ttgcgaccag	ctgtgtctcg	cgccgctctg	gcttatgggc	600
aggagcagag	gaaagggtct	gcaacagcag	ttcccccggt	cactcaaaat	gcggctgggt	660
ccaaaggccc	cacggcaatg	gtcttctctca	acatgggtgg	gccatcgaag	attgacgaag	720
tggaagattt	tctgagcaga	ttatttgtat	gcattcctca	atatgcccg	tgctaccacc	780
atgtatgagt	ctgacaaaact	ctctcttctc	ataccaggcc	gatggcgatc	tgattcctct	840
cggacgactt	caatcatacc	tccggcctct	catcgctaag	cgcagaaccc	caaagatcca	900
acggcaatac	tccgatattg	gtggagggtc	accgatcagg	aaatggtccg	agtatcagt	960
cgaggaaatg	tgcagattgc	tagacaaaat	caatcccga	acggctcctc	acaagcctta	1020
cgctcgcgtt	cggtagcggc	accctctgac	ggaagaaatg	tacacaaaat	tgctggaaga	1080
tggattcggc	aacgggaaaag	gcgggcgcgc	tgctcgcgtt	acacagtacc	cccaatattc	1140
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catgagtgtt	gtcaacagag	gtgagactca	tcttcttacc	gaacaacaag	atttgctcgc	1440
taacacattt	cctaggcgac	ccatatacct	ctgaagtgtg	tgcaactgtg	catgctgtca	1500
tgcaaagatt	gaatttcagc	aatccttacc	gactgtgctg	gcagtcccaa	gtgggaccgt	1560
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gttaagttgt	gttgtaaacg	aggtgaccca	ttcacggagc	acagcagagc	aatgtatata	2040
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atataaaaat	attaggaatg	aaggatttcc	gggtcaacct	ttgacaatta	ttttgccacc	2160
atttaacggt	gcacatatgc	aacgataaag	cacgacccag	tcgtagtgtt	ggtgtccctt	2220
atcgagaaat	tgcatgagat	tactccaacc	gctcaaaatc	tcaaaccctg	ataagaaaaa	2280
ttgattattg	aacaaactct	catagcgtcg	tttcgttaatt	actggttggt	cggaatcggg	2340
ctgacgcaaa	gccaacggc	cacgaagctg	ctccagctcc	gttcccagtt	ctcgtgaaga	2400
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<210> 108

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Genomic sequence containing the coding region

<400> 108

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gcaacagcag	ttcccccggt	cactcaaaat	gcggctgggt	ccaaaggccc	cacggcaatg	180
gtcttctctca	acatgggtgg	gccatcgaag	attgacgaag	tggaagattt	tctgagcaga	240

ttattttgat	gcatttccca	atatgcccga	tgctaccacc	atgtatgagt	ctgacaaaact	300
ctctcttctt	ataccaggcc	gatggcgatc	tgatttctct	cggacgactt	caatcatacc	360
tcggccctct	cacgctcagg	cgcagaaccc	caaagatcca	acggcaatac	tcggatattg	420
gtggaggggtc	accgatcagg	aaatgggtccg	agtatcagtg	cgaggaaatg	tgacagattgc	480
tagacaaaaat	caatcccga	acggctcctc	acaagcctta	cgtcgcgttc	cggtacgccg	540
accctctgac	ggaagaaatg	tacacaaagt	tgctggaaga	tggattcggc	aacgggaaag	600
gcggggcgcg	tgctgcgttc	acacagtacc	cccaatatct	gtgctccacc	acgggtagct	660
cgctgaacga	gttgtggaaa	tggagaacca	ggcttgaggg	taagcgtgca	aatggcaaca	720
tggaccccg	tgggtgccatc	cagtggagtg	tcatgatcg	atggccaacg	caccctggcc	780
tcgtggaggc	tttcgcccgg	aacattgagg	agcagctgaa	gacataacca	gaggagaagc	840
gaaacgggtg	cggttctctt	ttctcagccc	acagtctgcc	catgagtgtt	gtcaacagag	900
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ccatattctg	ctgaagtgtg	tgcaactgtg	catgtgttca	tgcaaaagatt	gaatttctagc	1020
aatccttacc	gactgtgctg	gcagtcctca	gtgggaccgt	cagcttggct	tggagcccaa	1080
actagcgata	cggctcgaaaa	ctatgtcaaa	cgtggacaga	ccgatattat	tctagttccc	1140
attgccttca	ccagcgacca	tattgagact	ctgtacgagt	tggatctgga	agtgataaag	1200
gaagcaaact	ccccgggagt	caagagagcc	gagagtttga	atggtaaccc	catttttcatt	1260
caggcattag	cagacattgc	ccaagagcac	ctccgtaagg	gagagaagtg	ctcactacag	1320
atgactctgc	gctgtcaagg	ctgtaagagc	gaacgggtgc	tggaaacagaa	gaaatttctt	1380
gctggcgacc	gattttcttc	tcttgtagtt	tag			1413

<210> 109

<211> 1287

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420

Coding region without exons

<400> 109

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gcaacagcag	ttcccccggt	cactcaaaat	gcggctgggt	ccaaaggccc	cacggcaatg	180
gtcttctctc	acatgggtgg	gccatcgaag	attgacgaag	tggaaagattt	tctgagcaga	240
ttatttgccg	atggcgatct	gattcctctc	ggacgacttc	aatcatacct	cggccctctc	300
atcgctaagc	gcagaacccc	aaagatccaa	cggcaatact	cggatattgg	tggaggggtca	360
ccgatcagga	aatgggtccga	gtatcagtg	gaggaaatgt	gcagattgct	agacaaaatc	420
aatcccgaaa	cggctcctca	caagccttac	gtcgcgttcc	ggtacgccga	ccctctgacg	480
gaagaaatgt	acacaaagtt	gctggaagat	ggattcggca	acgggaaagg	cgggcgcgct	540
gtcgcgttca	cacagtaccc	ccaatatctg	tgctccacca	cgggtagctc	gctgaacgag	600
ttgtggaaat	ggagaaccag	gcttgagggt	aagcgtgcaa	atggcaacat	ggaccccgct	660
ggtgccatcc	agtggagtgt	cattgatcga	tggccaacgc	accctggcct	cgtggaggct	720
ttcgcccggg	acattgagga	gcagctgaag	acataccag	aggagaagcg	aaacggtgtc	780
gttctcttgt	tctcagccca	cagtctgccc	atgagtgttg	tcaacagagg	cgacccatat	840
cctgctgaag	ttgctgcaac	tgtgcatgct	gtcatgcaaa	gattgaattt	cagcaatcct	900
taccgactgt	gctggcagtc	ccaagtggga	ccgtcagctt	ggcttggagc	ccaaactagc	960
gatacggctg	aaaactatgt	caaacgtgga	cagaccgata	ttattctagt	tcccattgcc	1020
ttcaccagcg	accatattga	gactctgtac	gagttggatc	tggaaagtgt	aaaggaagca	1080
aactccccgg	gagtcaagag	agccgagagt	ttgaatggta	accccatctt	cattcaggca	1140
ttagcagaca	ttgcccaaga	gcacctccgt	aagggagaga	agtgtcact	acagatgact	1200
ctgcgctgtc	aaggctgtaa	gagcgaacgg	tgcttggaa	agaagaaatt	ctttgctggc	1260
gaccgatatt	cttctcttgt	agtttag				1287

<210> 110

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Protein sequence

<400> 110

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Ala Cys Leu Gly Leu Arg Pro Ala Val Ser Arg Ala Ala Leu Ala Tyr
          20          25          30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
          35          40          45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
          50          55          60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
65          70          75          80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
          85          90          95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
          100          105          110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
          115          120          125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
          130          135          140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
145          150          155          160

Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
          165          170          175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
          180          185          190

Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
          195          200          205

Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
          210          215          220

Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
225          230          235          240

Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
          245          250          255

Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
          260          265          270

Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
          275          280          285

His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
          290          295          300

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Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
 385 390 395 400
 Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
 405 410 415
 Phe Phe Ala Gly Asp Arg Phe Ser Ser Leu Val Val
 420 425

<210> 111

<211> 2865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 111

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acaaggcggg	atcgtctttc	aacacgcggg	cggtgagctt	atcagcgccg	attgcggggg	180
ggtgcagcaa	atcaagtcag	tcgccacttt	cggcgaccat	gacaaagcgc	aagattgggt	240
ttactaaacc	gcctactttt	tttttatcaa	agagacttgg	gtttgtcagc	ttttctttat	300
cttctgaaag	agcgcttctc	tggtcaagct	gttcacaaaa	tccccatcac	tactgttccc	360
tttgtcggtt	ttttcgtcgc	attgcatcta	caacaaagaa	aacgggctcg	acgaaccctg	420
cgagatccat	acttctctgg	gtggcggtct	tcttagtcct	tatcgcatag	cggggtgctc	480
gaccagaagt	ccctgccacg	atgagtgcaa	tcctttctgc	agacgatttg	aacgatttca	540
tttctcccgg	ggttgcttgc	atcaagcccc	ttgagagtct	accacaaaaa	gaatcccagt	600
cggaggtatc	tttcctgtct	taccagtcac	ctgttgatat	cagccaatag	gctaacgctc	660
atttccaatt	caatagaatc	cctatgaggt	gacaaaggaa	gacaaagttc	aaccggaaaa	720
ccttcccccg	gtcagatatt	cattgactga	ttgccttgca	tgctccggat	gtgtcacgtc	780
tgcggaagca	gtgttgatat	ccttgcaatc	acatacgag	gttctcaata	ctcttgattc	840
gtaccccgaa	ttgcgcgttg	gttctacaag	ctaccaaaga	ggcacacaaa	aagttggatc	900
agcagacagc	gatggtcgca	tctttgttgc	tagcgtcagc	cctcaagtca	gggcgagctt	960
ggcagccaca	tacggaatca	ccgagcgggg	ggcgaaatat	atgattgacc	aatttcttat	1020
gggcctcac	ggtctcagag	ctggtggaaa	acatggcaat	gggtttacat	gggttggtgga	1080
cacgaacgtt	atgcgtgaag	cagtgtttgg	tctgacagcg	gacgaggtca	cgagctcttt	1140
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ctggatatgt	tatgctgaaa	aaacacaccc	ttttatcctt	ccgcatttat	ctcgcctcaa	1260
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acccgtccgc	gacgttgact	gtgtcataac	caccctgag	ctactaactt	tagccactgc	1500

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atcgggatga	caaagcagcc	tagagcattt	ggcagaaaaa	gtgctctacc	ccaagtctga	2820
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<210> 112

<211> 1865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Genomic sequence containing the coding region

<400> 112

atgagtgc	tcctttctgc	agacgatttg	aacgatttca	tttctcccg	ggttgcttgc	60
atcaagccc	ttgagagtct	accacaaaa	gaatcccagt	cggaggtatc	tttctgtct	120
taccagtc	ctgttgatat	cagccaatag	gctaacgctc	atttccaatt	caatagaatc	180
cctatgagg	gacaaaggaa	gacaaagttc	aaccggaaaa	ccttccccc	gctcagattt	240
cattgactga	ttgccttgca	tgtccggat	gtgtcacgtc	tgcggaagca	gtgttgatat	300
ccttgcaatc	acatacggag	gttctcaata	ctcttgattc	gtaccccgaa	ttgccgcttg	360
gttctacaag	ctaccaaaaga	ggcacacaaa	aagttggatc	agcagacagc	gatggctgca	420
tctttgttgc	tagcgtcagc	cctcaagtca	ggcgagctt	ggcagccaca	tacggaatca	480
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cagtgttggc	tctgacagcg	gacgagggtc	cgagctcttt	attatcaact	ggatcgggca	660
gccttcccaa	gagtccaatt	ctttcgtccg	cttgccccgg	ctggatatgt	tatgctgaaa	720
aaacacaccc	ttttatcctt	ccgcatttat	ctcgcctcaa	gtctcctcag	gcgttgagcg	780
gcacatttct	gaagtcagtg	ctaagcaagg	cacttggggt	cccgccttct	cagatatggc	840
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acattgcatg	ggcttcaacc	ttcaccaggt	cacagacaac	accgctccgc	gacgttgact	960
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cccagcgtgg	gcgcaacgcc	gatgttggtg	aatatgtgct	catgtcgtct	ggggatgagc	1260
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tggtgcacc	gaaacccacg	ccgcatgagc	agcgtgcctg	gctagcccgg	gtagatgaag	1620
cgtactactc	tgcggactcg	gatagcgagg	gatctgtcac	gacggagccg	gtttctgtcc	1680
tgtcaaggga	taaccagatt	catgagtttt	tgaactattg	gtcagagaag	gttgatatac	1740
ccctttccc	gctcgcgtac	acgtcctatc	gcgaagtggg	gagcgacgtg	ggtaagacga	1800
agaatgcgcc	caacgaaact	gctcgtgttg	tggaattggc	aggaaagatc	ggaggtggtt	1860
ggtga						1865

<210> 113

<211> 1725

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
Coding region without exons

<400> 113

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acaaaggaag	acaaagtcca	accggaatac	cttcccccg	ctcagatttc	attgactgat	180
tgccttgcat	gctccggatg	tgtaacgtct	gcggaagcag	tggtgatata	cttgcaatca	240
catacggagg	ttctcaatac	tccttgattcc	gatggtcgca	tccttggtgc	tagcgtcagc	300
cctcaagtca	gggcgagctt	ggcagccaca	tacggaatca	ccgagcggga	ggcgaaatat	360
atgattgacc	aattttcttat	gggccctcac	ggtctcagag	ctggtggaaa	acatggcaat	420
gggtttacat	gggttggtga	cacgaacggt	atgcgtgaag	cagtgttggc	tctgacagcg	480
gacgaggtca	cgagctcttt	attatcaact	ggatcgggca	gccttcccaa	gagtcgaatt	540
ctttcgtccg	cttgcccccg	ctggatatgt	tatgctgaaa	aaacacaccc	ttttatcctt	600
ccgcatttat	ctcgcctcaa	gtctcctcag	gcgttgagcg	gcacatttct	gaagtacgtg	660
ctaagcaagg	cacttggggt	cccgccttct	cagatatggc	atttagctat	catgccatgc	720
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cccgcgtcat	gtttaactcc	atttccagat	caagccctag	aatcattttt	gttctctaag	960
agctcgtcgg	gccaaacagt	cgaatcaggg	acatctggag	gctatcttca	tcacgtcctc	1020
caaactcttc	aagccagaaa	ccccggcgag	aagattgtca	cccagcgtgg	gcgcaacgcc	1080
gatgttggtg	aatatgtgct	catgtcgtct	ggggatgagc	ctcttttttag	ggcgggtcgg	1140
tattatgggt	tcaggaatat	acaaaatctc	gtcagaaaac	ttaaacccgc	acgcgtgtca	1200
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gttccgaacg	cactaaaaga	gacatcgact	gaaactcctg	tggtgcacc	gaaacccacg	1440
ccgcatgagc	agcgtgcctg	gctagcccgg	gtagatgaag	cgtactactc	tgcggactcg	1500
gatagcgagg	gatctgtcac	gacggagccg	gtttctgtcc	tgtcaaggga	taaccagatt	1560
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acgtcctatc	gcgaagtggg	gagcgacgtg	ggtaagacga	agaatgcgcc	caacgaaact	1680
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<210> 114

<211> 574

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
Protein sequence

<400> 114

Met Ser Ala Ile Leu Ser Ala Asp Asp Leu Asn Asp Phe Ile Ser Pro

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Gly Val Ala Cys Ile Lys Pro Val Glu Ser Leu Pro Gln Lys Glu Ser	20	25	30
Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro	35	40	45
Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys	50	55	60
Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser	65	70	75
His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val	85	90	95
Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly	100	105	110
Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly	115	120	125
Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp	130	135	140
Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala	145	150	155
Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro	165	170	175
Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala	180	185	190
Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser	195	200	205
Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala	210	215	220
Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys	225	230	235
Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala	245	250	255
Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val	260	265	270
Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg	275	280	285
Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys	290	295	300
Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys	305	310	315
Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu	325	330	335

His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365
 Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser
 500 505 510
 Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
 515 520 525
 Glu Lys Val Asp Ile Pro Leu Ser Arg Leu Ala Tyr Thr Ser Tyr Arg
 530 535 540
 Glu Val Glu Ser Asp Val Gly Lys Thr Lys Asn Ala Pro Asn Glu Thr
 545 550 555 560
 Ala Arg Val Val Glu Leu Ala Gly Lys Ile Gly Gly Gly Trp
 565 570

<210> 115

<211> 1510

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 115

taagagttgc aggtatgagc ctggtaaatc aagtcagtca cggatagcac aacagaacct	60
cattttgtcc tgaagaatg aaccaaaaagg ccaactcaga ctctttgcaa atgcaaggaa	120
gaggtaatga gaatgttttg ggagaagctt aaatgtagct ttgccggaac ggagaattga	180
gtaaagccgg tcatgaggcg ccaagacccc agcgaaaaag cagccctagg ccgcacgcaa	240

```

ccccgttcgg cgagttgcta ctggctgtta agcgagactc ttgtgggcga agaccgcaac 300
acccgaaatt cgcgatccag tagcccagag cgacttgtgt gcgtttcggg cgactttgac 360
aatcccgaact cttcgacaac aaattcccat caccgccctc ccggagtctg tcgaccgtga 420
gttttgaaacc ttacgccctat cgaatttctg gactgtcact gaagaatccg tttttgtcgt 480
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ttgaggttgg ccgtgttgtg ctgatccgca gcggtcctta caccggcaag cttgctgcca 600
ttgtcgagat catcgaccac aagcgtgtac gtttttcaac ggagaaattc tgagcgcagg 660
acggaaagat catggtcgga tgtgatattg acaaagaggc gcgatcatag gtcctggttg 720
acggtccttc caccgaggag aacaagatcg ttccccgtca cgctcttcct ctcgctcacg 780
ccactctcac ccccttcgtc attcccaaac tccccgcgc tgccggcact ggccccgtca 840
agaagctctg ggagaagaac gagatcgatg gaaagtgggc taagagcacc attgctcaga 900
agactgagcg cgctgagcgg aggaagaacc ttaccgactt cgagcgcttc aaggtcctca 960
gactcaagaa gcaggtacgt tcagtttgcg aaactatggg agaattgtga tggcacattg 1020
gagggcattc ttggcaactc tgcaactcgt tttcgcgaga gggaagagga gcaattactt 1080
gtattatgat ttgcgactgg ttactgacat ctggtgattt aacaggctcg ctacgaggtc 1140
cagaaggctc acgccaaggt cagggctgct gctcctaagt catagatgtt ttcagaggtc 1200
tcggtgcata gtatgaaggg gtaccttggg acggttttac atggctgagg gttttattct 1260
atttcagcaa aaattaagct gtatccacta caatgacagc caaaaaatga ttcaaacct 1320
tgatatcctg acacgggtca tctgctatg tcatcagatt cgcgcacccg attagtactt 1380
ggctctgggt tatagccgtc tccttagaca ttaattggga attaaacatt ttagactcaa 1440
gatcacgga tatgtaagaa agtatcgta tgtacattac tgagttggat tggctcgta 1500
tgactcgat 1510

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<210> 116

<211> 685

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Genomic sequence containing the coding region

<400> 116

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ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
aagcgtgtac gtttttcaac ggagaaattc tgagcgcagg acggaaagat catggtcgga 180
tgtgatattg acaaagaggc gcgatcatag gtcctggttg acggtccttc caccgaggag 240
aacaagatcg ttccccgtca cgctcttcct ctcgctcacg ccactctcac ccccttcgtc 300
attcccaaac tccccgcgc tgccggcact ggccccgtca agaagctctg ggagaagaac 360
gagatcgatg gaaagtgggc taagagcacc attgctcaga agactgagcg cgctgagcgg 420
aggaagaacc ttaccgactt cgagcgcttc aaggtcctca gactcaagaa gcaggtacgt 480
tcagtttgcg aaactatggg agaattgtga tggcacattg gagggcattc ttggcaactc 540
tgcaactcgt tttcgcgaga gggaagagga gcaattactt gtattatgat ttgcgactgg 600
ttactgacat ctggtgattt aacaggctcg ctacgaggtc cagaaggctc acgccaaggt 660
cagggctgct gctcctaagt catag 685

```

<210> 117

<211> 465

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Coding region without exons

<400> 117

```

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ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
aagcgtgtcc tgggtgacgg tccttccacc gaggagaaca agatcgttcc ccgtcacgct 180
cttctctcgc ctcacgccac tctaccccc ttcgtcattc ccaaactccc ccgcgctgcc 240

```



```

ggcactggcc ccgtaagaa gctctgggag aagaacgaga tcgatggaaa gtgggctaag 300
agcaccattg ctcagaagac tgagcgcgct gagcggagga agaacccttac cgacttcgag 360
cgcttcaagg tcctcagact caagaagcag gctcgctacg aggtccagaa ggctcacgcc 420
aaggtcaggg ctgctgctcc taagtcatag atgttttcat gaggc 465

```

<210> 118

<211> 149

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Protein sequence

<400> 118

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Met Ala Asp Ile Asp Val Lys Val Ala Gln Trp Lys Leu Val Glu Val
1           5           10           15

```

```

Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala
          20           25           30

```

```

Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
          35           40           45

```

```

Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
          50           55           60

```

```

His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
          65           70           75           80

```

```

Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
          85           90           95

```

```

Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
          100          105          110

```

```

Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
          115          120          125

```

```

Lys Gln Ala Arg Tyr Glu Val Gln Lys Ala His Ala Lys Val Arg Ala
          130          135          140

```

```

Ala Ala Pro Lys Ser
145

```

<210> 119

<211> 1942

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 119

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gtctctggcc gaactctggt ctaatttcct agagcaggag tcacaggcca gtgggaatcc 120
agaatcgccg aaaccatgaa gagtttcaaa aggtggctct gttctgagcc gtatagaaaa 180
ctagcatctt ctctaagata cggtggttcc acatttatat atgcttgccg actggctttg 240

```

```

gtctcctctt cttttccatt ctagacttgc ttcgtagtaa taacactgat atcacccgcg 300
tgtttgcgac ttttgcacat aaccagcttc cccaccgctt tctttctgcc accatagcgg 360
gggaacctcgt tattgagcgg acaagtcgtc gttggctttt tctgcacggt tggcctatgc 420
ttcgttttatt cagctctggt acagctggga agttgactga tacactctcc tctctgattt 480
cttgggtaact cagattgaca atgactaccg gggctggtac gatctctcat tccaacacct 540
atcatcgtat tcctcgccgt taactgacca atccaccagt gcaaagggtt cgtccagtgg 600
tggtatcggg tccctctggg actgggaagt cgaccttgct caagagactc ttcgctgaat 660
accccgatac tttcgattta tccgtgtctc gtacgtctaa ccccttgcca accctcattg 720
actatgcctg cgaattgttt cttttggtgg aattgcgctg aacggtgttt gttatatatta 780
gataccactc gagctccccg tcccggggaa gaaaatggac gtgagtatta cttcacaact 840
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cgtagatact gtcggttcg atactgaaaa caatgcacga tctgccttgg taacttcggt 1560
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gacaaatcta ggaagggtg tagactcagt cactctcttg aacggagagg agaaaattaa 1740
gcaaaactaa aaaagagaac aaagtctgat gagcaatatg agggctgaaa aggatatctg 1800
taaagaggct gctagaataa aatggaagat gccgattgag aaggcaatgg aggaagagaa 1860
gggggtcattt atcgcagttt gggcgtggac cagaaatgac tgcagtatgt ttatggacca 1920
tgccagccgg agctattgga ct 1942

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<210> 120

<211> 943

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Genomic sequence containing the coding region

<400> 120

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atgactaccg gggctggtac gatctctcat tccaacacct atcatcgtat tcctcgccgt 60
taactgacca atccaccagt gcaaagggtt cgtccagtgg tggtatcggg tccctctggg 120
actgggaagt cgaccttgct caagagactc ttcgctgaat accccgatac tttcgattta 180
tccgtgtctc gtacgtctaa ccccttgcca accctcattg actatgcctg cgaattgttt 240
cttttggtgg aattgcgctg aacggtgttt gttatatatta gataccactc gagctccccg 300
tcccggggaa gaaaatggac gtgagtatta cttcacaact aaagaagatt tcctggatct 360
tgtgagcaag aatgccttta tcgagcatgc gcagtttggg ggcaattact acggtactac 420
tgtgcaggca gtgaaggatg ttgcgagaa gggcaagatc tgcgttctcg acattgagat 480
ggaggtataa atagtcctgc aacgtgaact gatatgaccg gagaagcaga ggaaatccat 540
catcaaattg attgtagttc aacccaaaca acagctgacg actgaattgc aatagggcgt 600
gaaacaagtc aagcgcaccg atcttgatgc tcgattctta tttttagcac ccccgctcct 660
tgaagaacta gagaaaagac tgcgtgggag agcaaccgag actgaggaga gcttgacggg 720
atggctgtcc tccacattcc ttcacttccc caactcgcca gactgtcccc ctggaattct 780
aactttgcgt cagaaaacgcc ttgcccagc taaaaatgaa ttggaatatg cggcgagcc 840
tggtctctcat gataagattg tcgtgaacga tgacctggag aaggcttata aggaactgcg 900
ggattggatt gtcgacgggt gtaactttgg agcgcgtcaa tga 943

```

<210> 121

<211> 603

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Coding region without exons

<400> 121

```

atgactaccg gggctgtgca aaggttccgt ccagtgggtg tatcgggtcc ctctgggact    60
gggaagtgcg ccttgctcaa gagactcttc gctgaatacc ccgatacttt cgatttatcc    120
gtgtctcata ccactcgagc tccccgtccc ggggaagaaa atggacgtga gtattacttc    180
acaactaaag aagatttcct ggatcttgtg agcaagaatg cctttatcga gcatgcgcag    240
tttgggtggc attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc    300
aagatctgcg ttctcgacat tgagatggag ggcgtgaaac aagtcaagcg caccgatctt    360
gatgctcgat tcttattttt agcaccctcg tcccttgaag aactagagaa aagactgcgt    420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgcccaagc taaaaatgaa    480
ttggaatatg cggcgagcgc tggctctcat gataagattg tcgtgaacga tgacctggag    540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaactttgg agcgcgtcaa    600
tga                                                    603

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<210> 122

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Protein sequence

<400> 122

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Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
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Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
20          25          30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
35          40          45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
50          55          60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
65          70          75          80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
85          90          95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Glu Gly Val
100         105         110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
115         120         125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
130         135         140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
145         150         155         160

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Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
165 170 175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
180 185 190

Gly Gly Asn Phe Gly Ala Arg Gln
195 200

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<210> 123
<211> 3108
<212> DNA
<213> Aspergillus fumigatus
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<220>
<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
      Genomic sequence containing 3' and 5'-ends and the coding region
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gtagatacat	gctgaggcac	aggatggttg	agtggagggtg	actgcgcagg	cggtggtgcg		180
aaagactggc	ggtacatggt	gatttttttt	tcccttggtta	caataagtga	gaagctagtgtg		240
atgaacaaaa	gacttgcgac	tattctgtct	cgtcttcttg	tcttctacca	accgaagagg		300
ggggatgttg	gaaatcggac	agtttgagta	tgagtgatgt	tgaagtgtgt	ttatacgtgg		360
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gtggccacta	cacacacttg	tccgttctcc	aaaaccacg	ctgctcgcac	tgaataatat		480
acacaagaag	tgtttacaac	atgttagaag	ccttcgaagt	cttgacaaca	tctgggggtgg		540
tgctgtggtc	gaagtcgtat	gcgcgggtcg	gagcgcgatgt	tgtcaacagc	ctaatacaacg		600
atgtcttcat	tgaggagaag	gttcgagcgc	agaatcaggc	agcgagcagt	gcagctccta		660
tctacaagaa	ggaaaagtat	actctgaaat	ggaagcaagt	aaaggatttc	aatctgatata		720
ttgtggtatg	ttcacgccgc	tcgttgattc	aatggcgcca	ctgaccgatt	ccataggctg		780
tatatcaatc	tctgtatcat	cttggttgga	tcgacaaact	cttgataat	gtttcgacca		840
tattcatcga	cttatataag	gatgagctaa	ggagcacacg	ggctaggatt	attgagtacc		900
cattcgataa	gtacttcgac	cagcaggtgc	gagagcttga	ggacaatgct	ggggctccta		960
catcagaatc	tctcgtagta	gagatcaacg	agagaaagga	ccctcttgct	tcatcagata		1020
acggcggggc	acctccgcc	cccgtgcctg	gtctgctgaa	aggtatctga	cgtcgataat		1080
ttttctctgc	tagtgatcat	attgctaact	acctccgaag	cgcaacgtcc	agttgocgag		1140
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cgcgcacgca	aagcggccaa	cgcgacgcgt	accgctctct	ctggagatga	aagcattcgg		1320
aaagggaaaa	cattgaaaag	tggaaaaaag	atgcgcaagt	gggatgctga	tggctttgcg		1380
gatgaggacg	acggcaaggt	cctcgattac	tccgcccccg	cgatgggtga	ggacgcaccg		1440
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atcatcagta	aatgtgatac	cgttggtgac	atggtaggta	cgcttgctcag	catggtgcat	2460
gctacaggca	ttcctattgt	ttttctgggt	gtaggccagc	actatggtga	tttgaggggc	2520
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tcttgatccg	tagtcaagcg	ccttaccatt	gggccagcag	gccttcttga	aggttttcac	2820
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<210> 124

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
 Genomic sequence containing the coding region

<400> 124

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gttcgagcgc	agaatcaggc	agcgagcagt	gcagctccta	tctacaagaa	ggaaaagtat	180
actctgaaat	ggaagcaagt	aaaggatttc	aatctgatat	ttgtggtatg	ttcacgccgc	240
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cttggttgga	tcgacaaaact	cttggataat	gtttcgacca	tattcatcga	cttatataag	360
gatgagctaa	ggagcacacg	ggctaggatt	attgagtacc	cattcgataa	gtacttcgac	420
cagcaggtgc	gagagcttga	ggacaatgct	ggggctccta	catcagaatc	tctcgtagta	480
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cccgtgcctg	gtctgctgaa	aggtatctga	cgctcgataat	ttttctctgc	tagtgatcat	600
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caaccaagct	ttcggcactg	ggagaaacct	cgatgggttc	atcatcagta	aatgtgatac	1920
cgttggtgac	atggtaggta	cgcttgctcag	catggtgcat	gctacaggca	ttcctattgt	1980
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<210> 125
 <211> 1884
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
 Coding region without exons

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gttcgagcgc agaatcaggc agcgagcagt gcagctccta tctacaagaa ggaaaagtat    180
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acacgggcta ggattattga gtaccattc gataagtact tcgaccagca ggtgcgagag    360
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aaggaccctc ttgtctcatc agataacggc gggccacctc cgccacccgt gcctgcctcg    480
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catctattga ccgcgaaaag agggcctgct ggccgcgcct ctcgtcgcgc acgcaaagcg    600
gccaacgcga gcgctaccgc ttcttctgga gatgaaagca ttcggaaggg gaaaacattg    660
aaaagtggaa aaaagatgcg caagtgggat gctgatggct ttgcggatga ggacgacggc    720
aaggctcctc attactccgc cccgcgagat ggtgaggacg caccggctcc tgtagtcgag    780
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cgtcataacg accaacgcct tatgtcttcg ctcgagaagt tcgccaagtt cgccaaacca   1620
gataagatct tcatggtcgg tgaagctctg gtcggtacgg acagcgtgat gcaggctcgc   1680
aacttcaacc aagctttcgg cactgggaga aacctcgatg ggttcatcat cagtaaatgt   1740
gataccgttg gtgacatggg aggtacgctt gtcagcatgg tgcattgctac aggcattcct   1800
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<210> 126
 <211> 641
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
 Protein sequence

<400> 126

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Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile
          20          25          30
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Asn	Asp	Val	Phe	Ile	Glu	Glu	Lys	Val	Arg	Ala	Gln	Asn	Gln	Ala	Ala	
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Ser	Ser	Ala	Ala	Pro	Ile	Tyr	Lys	Lys	Glu	Lys	Tyr	Thr	Leu	Lys	Trp	
	50					55					60					
Lys	Gln	Val	Lys	Asp	Phe	Asn	Leu	Ile	Phe	Val	Ala	Val	Tyr	Gln	Ser	
65					70					75					80	
Leu	Leu	His	Leu	Gly	Trp	Ile	Asp	Lys	Leu	Leu	Asp	Asn	Val	Ser	Thr	
				85					90					95		
Ile	Phe	Ile	Asp	Leu	Tyr	Lys	Asp	Glu	Leu	Arg	Ser	Thr	Arg	Ala	Arg	
			100					105					110			
Ile	Ile	Glu	Tyr	Pro	Phe	Asp	Lys	Tyr	Phe	Asp	Gln	Gln	Val	Arg	Glu	
		115					120					125				
Leu	Glu	Asp	Asn	Ala	Gly	Ala	Pro	Thr	Ser	Glu	Ser	Leu	Val	Val	Glu	
	130					135					140					
Ile	Asn	Glu	Arg	Lys	Asp	Pro	Leu	Val	Ser	Ser	Asp	Asn	Gly	Gly	Pro	
145					150					155					160	
Pro	Pro	Pro	Pro	Val	Pro	Val	Ala	Gln	Gly	Val	Ala	Thr	Ser	Asp	Glu	
				165					170					175		
Gly	Ser	Pro	Pro	Gln	Thr	Pro	Asp	Leu	Ser	Arg	Ser	Ser	Thr	Pro	Ile	
			180					185					190			
Ser	Gly	His	Leu	Leu	Thr	Ala	Lys	Gly	Gly	Pro	Ala	Gly	Arg	Ala	Ser	
		195					200					205				
Arg	Arg	Ala	Arg	Lys	Ala	Ala	Asn	Ala	Ser	Ala	Thr	Ala	Ser	Ser	Gly	
	210					215					220					
Asp	Glu	Ser	Ile	Arg	Lys	Gly	Lys	Thr	Leu	Lys	Ser	Gly	Lys	Lys	Met	
225					230					235					240	
Arg	Lys	Trp	Asp	Ala	Asp	Gly	Phe	Ala	Asp	Glu	Asp	Asp	Gly	Lys	Val	
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Leu	Asp	Tyr	Ser	Ala	Pro	Ala	Asp	Gly	Glu	Asp	Ala	Pro	Ala	Pro	Val	
			260					265				270				
Val	Glu	Ala	Val	Ala	Gln	Glu	Ser	Trp	Gly	Arg	Arg	Thr	Gly	Lys	Gly	
		275					280					285				
Gln	Phe	Val	Leu	Lys	Asp	Leu	Gly	Asp	Glu	Val	His	Ser	Ile	Leu	Glu	
	290					295					300					
Asn	Ala	Asp	His	Glu	Lys	Thr	Lys	Ser	Ser	Ser	Ser	Thr	Gly	Phe	Val	
305					310					315					320	
Gly	Ser	Gly	Val	Asn	Ala	Leu	Gly	Gly	Phe	Phe	Arg	Asn	Ile	Val	Gly	
				325					330					335		
Gly	Lys	Val	Leu	Thr	Glu	Ala	Asp	Leu	Glu	Lys	Pro	Leu	Lys	Ala	Met	
			340					345					350			
Glu	Asp	His	Leu	Leu	Lys	Lys	Asn	Val	Ala	Arg	Glu	Ala	Ala	Val	Arg	

355	360	365
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Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile 405 410 415		
Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr 420 425 430		
Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu 435 440 445		
Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile 450 455 460		
Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val 465 470 475 480		
His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu 485 490 495		
Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala 500 505 510		
Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu 515 520 525		
Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser 530 535 540		
Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val 545 550 555 560		
Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe 565 570 575		
Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser 580 585 590		
Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val 595 600 605		
His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr 610 615 620		
Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met 625 630 635 640		
Lys		

<210> 127

<211> 2564

<212> DNA

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 127

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gatgattccg	attattgtga	aactgggtta	aatcgcgcca	gaggggcagg	tatcgtgacg	240
gagagggggg	atatcgtcga	atggagggtg	tgagtgcga	cggccgacga	ttgcgcagtt	300
caaagcggcg	aagaggtctt	ggcactctcg	gtccaaacac	gttgcccgtt	ctctccaact	360
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ctattccttc	tctttctccg	gactgcagtg	acttcccttt	cagccaattg	cccgtctccac	480
tgtgcggcat	tcgatatacc	atgcggtggt	gcctcactct	tctggcattc	tgcttcttgg	540
cagttgtacg	tgcattaagt	agctccggca	gtcgtctggt	ggttggtttg	gaagatgcca	600
cagaaaagga	attatactcg	aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	660
cttctacgtt	aatatgctaa	tattaattgg	tagctcgagg	atataacctc	gacttcgaat	720
cccccaagaa	tgacaagctc	agcctgttcg	aactcggaga	ccgagtctac	gaccacatgc	780
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cctctgtcac	cgtcgatcac	ttcaactacg	atacactttc	tgctccgat	aagcatgatg	1080
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atttccacgg	aatcgctttc	gcattgtgat	caaccacgcg	ctagattgtg	cccgttgtca	2520
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<210> 128

<211> 1564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Genomic sequence containing the coding region

<400> 128

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aagggttagc	gttaccctta	gacatgtcca	tatgctctgc	tttgtagatc	tcaattgacc	360
tcttgccag	gctatggacc	ctcccttacc	cccaagaata	tcattgattt	catgaacaag	420
gacggtaacg	tcctcctcgc	cttgctgggc	aagtccacaa	ccgccagcgc	tatcagctcg	480
ctgctattgg	agctcgatct	ccatctccct	gtcgatcggt	cctctgtcac	cgctgatcac	540
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ggcaagttga	ggtccgatac	caaggctttc	tttgatggcg	agggcggtgt	agcatttccc	660
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gatggtgaaa	tcactcccga	gaagctgaac	cctaagatct	atcgaataaa	gaatgaaact	1080
gtaagtgaca	gccatctgag	gttccattgc	ctatttgcat	gtcaccctt	ctcaacaggt	1140
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cagcgggtgga	tgggtctgga	ttgcgggtct	gtgggtccgtc	atcgctggct	tcttagtatt	1500
cgttgttgca	tggctttact	cagcgccttc	tgccgcccga	ctgaacacaa	agaagacaca	1560
ataa						1564

<210> 129

<211> 1383

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Coding region without exons

<400> 129

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ctcagcctgt	tcgaactcgg	agaccgagtc	tacgaccaca	tgcttctcct	gcctcccaag	240
tcaaagggct	atggaccctc	ccttaccccc	aagaatatca	ttgatttcat	gaacaaggac	300
ggtaacgtcc	tcctcgcctt	gtcgggcaag	tccacaaccg	ccagcgctat	cagctcgctg	360
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aactacgata	cactttctgc	ctccgataag	catgatgttc	tgctactcca	ccgaccaggc	480
aagttgaggt	ccgataccaa	ggctttcttt	gatggcgagg	gcgttgtagc	atttcccaga	540
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taa 1383

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<210> 130
<211> 460
<212> PRT
<213> Aspergillus fumigatus
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<220>
<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
      Protein sequence
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<400> 130															
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Ala	Thr	Glu 35	Lys	Glu	Leu	Tyr	Ser 40	Lys	Leu	Trp	Ala	Asp 45	Leu	Glu	Gly
Tyr	Asn 50	Leu	Asp	Phe	Glu	Ser 55	Pro	Lys	Asn	Asp	Lys 60	Leu	Ser	Leu	Phe
Glu 65	Leu	Gly	Asp	Arg	Val 70	Tyr	Asp	His	Met	Leu 75	Leu	Leu	Pro	Pro	Lys 80
Ser	Lys	Gly	Tyr	Gly 85	Pro	Ser	Leu	Thr	Pro 90	Lys	Asn	Ile	Ile	Asp 95	Phe
Met	Asn	Lys	Asp 100	Gly	Asn	Val	Leu	Leu 105	Ala	Leu	Ser	Gly	Lys 110	Ser	Thr
Thr	Ala	Ser 115	Ala	Ile	Ser	Ser	Leu 120	Leu	Leu	Glu	Leu	Asp 125	Leu	His	Leu
Pro	Val 130	Asp	Arg	Ser	Ser	Val 135	Thr	Val	Asp	His	Phe 140	Asn	Tyr	Asp	Thr
Leu 145	Ser	Ala	Ser	Asp	Lys 150	His	Asp	Val	Leu	Leu 155	Leu	His	Arg	Pro	Gly 160
Lys	Leu	Arg	Ser	Asp 165	Thr	Lys	Ala	Phe	Phe 170	Asp	Gly	Glu	Gly	Val 175	Val
Ala	Phe	Pro	Arg 180	Ala	Val	Pro	His	Thr 185	Leu	Gly	Asp	Ala	Asn 190	Pro	Leu
Ile	Ala	Pro 195	Ile	Leu	Arg	Ala	Pro 200	Ala	Thr	Ala	Tyr	Ser 205	Tyr	Asn	Pro
Lys	Glu 210	Asp	Ala	Ser	Ser	Val 215	Glu	Asp	Val	Ala	Ala 220	Thr	Gly	Ser	Gln
Leu 225	Ala	Leu	Val	Ser	Ala 230	Met	Gln	Ala	Arg	Asn 235	Ser	Ala	Arg	Phe	Thr 240
Leu	Leu	Gly	Ser	Val 245	Glu	Ser	Leu	Gln	Asp 250	Gln	Trp	Phe	Ser	Ala 255	Thr

Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu
 260 265 270

Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu
 275 280 285

Lys Val Gly Lys Ile Glu His His Leu Ala Glu Asp Gly Glu Ile Thr
 290 295 300

Pro Glu Lys Leu Asn Pro Lys Ile Tyr Arg Ile Lys Asn Glu Thr Val
 305 310 315 320

Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe
 325 330 335

Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser
 340 345 350

Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser
 355 360 365

Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
 370 375 380

Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu
 385 390 395 400

Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
 405 410 415

Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser
 420 425 430

Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala
 435 440 445

Pro Ser Ala Ala Ala Leu Asn Thr Lys Lys Thr Gln
 450 455 460

<210> 131

<211> 3376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 131

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gggcaggaga	aacgtaacgc	cggcgagtc	ccttttgagt	cagatgcccc	tctgtactat	420
tcaattttcg	gggaattcaa	cagcccactt	gttacgctct	cgcaggtcga	tttcaactcg	480
ggcgattttt	gagggccgca	atgtctcagt	atcagcttac	tgtggccacc	agggccaatc	540

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gaagcactga	aagagaattc	aattttacatt	gttaggatgc	taaatcgctg	atttacgaca	3000
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<210> 132

<211> 2376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
 Genomic sequence containing the coding region

<400> 132

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60

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<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Coding region without exons

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<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Protein sequence

<400> 134

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Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
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Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
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<211> 3639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
 Genomic sequence containing 3' and 5'-ends and the coding region

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<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

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<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
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 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
 Coding region without exons

<400> 137

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<210> 138
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 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
 Protein sequence

<400> 138

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 35 40 45
 Leu Ala Leu Cys His Leu Gln Asn Gly Gln Val Lys Ala Ala Tyr Asp
 50 55 60
 Tyr Ser Arg Asn Phe Gly Ser Arg Gly Thr His Leu Gly Cys Ser Tyr
 65 70 75 80
 Val Phe Ala Gln Ala Cys Leu Asp Leu Gly Lys Tyr Leu Glu Gly Ile
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 Thr Ala Leu Glu Arg Ser Lys Gly Leu Trp Ala Ser Lys Asn His Trp
 100 105 110
 Asn Lys His Ser Glu Thr Arg Arg Gln His Leu Pro Asp Ala Ala Ala
 115 120 125
 Val Phe Cys Leu Leu Gly Lys Leu Trp His Ala His Lys Asp Ile Asn
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 Lys Ala Val Glu Cys Tyr Val Glu Ser Leu Lys Leu Asn Pro Phe Met
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 Trp Asp Ala Phe Gln Gly Leu Cys Asp Thr Gly Val Asn Val Arg Val
 165 170 175
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 Ser Pro Gln Ala Asp Ala Glu Pro Ile Ser Asp Lys Ser Ala His Thr
 195 200 205
 Asn Gly Pro Leu Gln Ala Gln Ala Asn Val Asn Pro Ser Ser Asp Pro
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 245 250 255
 Ser Gly Val Pro Ala Ser Ile Val His Glu Gly Ala Glu Thr Pro Ser
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 Gly Gln Ser Ser Gly Ser Asp Glu Phe Arg Leu Ala Asn Gly Met Asn
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 Arg Thr Ile Gln Ala Ile Ser Gly Glu Tyr Pro Met Asp Pro Pro Pro
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<210> 139
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<213> Aspergillus fumigatus
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<220>
<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Genomic sequence containing 3' and 5'-ends and the coding region
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<210> 140

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
 Genomic sequence containing the coding region

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<210> 141

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Coding region without exons

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gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
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<210> 142

<211> 568

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Protein sequence

<400> 142

Met	Ala	Lys	Ala	Leu	Asp	Ile	Ser	Leu	Val	Thr	Thr	Gly	Val	Lys	Trp	1		5		10					15
Glu	Leu	Gln	Tyr	Asp	Val	Leu	Gln	Leu	Ser	Asp	Arg	Val	Asn	Glu	Leu			20		25				30	
Asn	Ser	Leu	His	Gly	Thr	Arg	Asp	Leu	Leu	Glu	Lys	Ile	Lys	Gln	Met		35		40				45		
Pro	Val	Thr	Leu	Pro	Glu	Asp	Thr	Leu	Glu	Thr	Tyr	Glu	Phe	Asn	His		50		55			60			
Leu	Leu	Arg	Asn	Val	Lys	Glu	Ala	Thr	Leu	Val	Leu	Arg	Asn	Met	Val	65		70		75					80
Leu	Leu	Lys	Glu	Asn	Ala	Tyr	Tyr	Val	Ser	Arg	Tyr	Ala	Lys	Gly	Leu			85		90				95	
Leu	Arg	Asp	Phe	Leu	Val	Ile	Met	Ile	Asn	Leu	Pro	Asn	Gln	Pro	Arg		100		105				110		
Leu	Asn	Glu	Ile	Lys	Asn	Asp	Ala	Leu	Asp	Ile	Ala	Glu	Glu	Val	Thr		115		120				125		
Lys	Phe	Met	Lys	Thr	Asp	Pro	Glu	Asp	Pro	Leu	Trp	Ile	Ser	Leu	Leu		130		135			140			
Asn	Cys	Leu	Gly	Ser	Ser	Asp	Arg	Ala	His	Val	Val	Arg	Ala	Leu	Trp	145		150		155					160
Ala	Leu	Thr	His	Phe	Ser	Thr	Glu	Leu	Asp	Glu	Pro	Glu	Ala	Asn	Arg			165		170				175	
Ala	Met	Glu	Arg	Ile	Pro	Lys	Glu	Thr	Leu	Gln	Gln	Leu	Tyr	Phe	His		180		185				190		
Thr	Leu	Leu	Asp	Leu	Asp	Lys	Asp	Ile	Leu	Ser	Gly	Ala	Leu	Asp	Phe		195		200			205			
Trp	Tyr	Gln	Tyr	Thr	Leu	Ser	Ser	Glu	Asn	Ile	Glu	Thr	Leu	Ile	Glu		210		215			220			
Val	Phe	Asn	Leu	Pro	Thr	Val	Phe	Val	Pro	Arg	Met	Val	Ala	Leu	Leu	225		230		235					240
Thr	His	Glu	Gly	Arg	Pro	Asn	Lys	Lys	Glu	Thr	Val	Leu	Gln	Glu	Glu			245		250			255		
Lys	Val	Ala	Pro	Pro	Pro	Ser	Asp	Ile	Pro	Arg	Val	Pro	Pro	Glu	Leu		260		265				270		
Met	Lys	Glu	Leu	Met	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Ser	Ser	Arg	Trp		275		280			285			
Leu	Arg	Cys	Cys	Phe	Val	Glu	Asp	Leu	Glu	Cys	Glu	Ile	Thr	Gln	Ile		290		295			300			
Ala	Leu	Trp	Gln	Ala	Tyr	Gln	Ser	Arg	Phe	Ala	Asp	Pro	Arg	Leu	Pro	305		310		315					320

Gly Gly Gly Val Leu Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr
 325 330 335
 Thr Phe Thr Asn Ala Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala
 340 345 350
 Thr Lys Phe Ile Ile Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr
 355 360 365
 Phe Glu Gly Phe Pro Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys
 370 375 380
 Pro Ser Lys Thr Cys Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg
 385 390 395 400
 His His Val Phe Thr Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro
 405 410 415
 Gly His Tyr Asn Leu Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu
 420 425 430
 Trp Asp Asn Cys Thr Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr
 435 440 445
 Ala Met Val Ala Gly His Val Ser Ala His Leu Pro Glu Glu Arg Ala
 450 455 460
 Pro Asp Ala Glu Pro Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg
 465 470 475 480
 Ile Val Arg Lys Trp Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly
 485 490 495
 Glu Pro Phe Gly Val Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu
 500 505 510
 Ala Arg Asn Leu Pro Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser
 515 520 525
 Trp Lys Lys Ala Val Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala
 530 535 540
 Trp Asp Arg Asn Arg Ser Leu Arg Lys Glu Leu Thr Glu Leu Ile Met
 545 550 555 560
 Val Ile Glu Lys Glu Asp Tyr Tyr
 565

<210> 143

<211> 2542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 143

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 gtctagtgtc atctccttcc acgtttccaa ttatcttctc ttttccttcc aaaaaaatta 120

aaaagcagat	actctcgtct	gctagaccgc	atactttgac	cggatcgggt	atcttccagt	180
acgagggtgc	tccgcatata	gtcacaattc	ctttttcaag	aggctttttc	ctcctctccc	240
tatccttttc	ccctccctag	catccccttc	gagcttgcc	taatttcgtc	catctggcct	300
gtgtgccatt	ctcttcattg	cgatcaagg	ccttctctct	caggcggaca	cagccccct	360
gttcgtctgg	gcagcagata	gtgcttccta	ggcttctgtg	tctacgggtc	actacatata	420
caccactgcg	ttgctcctca	tctcaataat	cggctctgca	ccagcatacg	tcacacaatt	480
cattacgtca	atcagcggaa	atggtctaca	tccgcatccc	caagaactac	acggcttcgc	540
cgtcttcctt	tgccggaact	ccgtccttga	cgatcaatta	cgaggcaacg	caggatcttg	600
attctaccaa	tgcttttgaa	ggtttggtga	cgccgggtgac	acgtgtgaga	gcagcgctgg	660
acagaggctg	acagtctaca	ggtccagaga	aactcttgga	ggtgtggttc	gcgccttccg	720
ctcaggaatt	aggtccagcg	cagcccgcgc	gtctgaaggc	tgttccggag	gagatctgga	780
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cttgtgttac	caccactctt	ctgtctggtc	tcacacgc	tctcgagatt	gccgctttgt	960
tcggtggctt	cccccaagtct	accgcccctt	ctcgcggaat	ctccgtcgcc	gctgcgcctt	1020
accgctctt	ctacagccgc	aagaacttcc	tggtccccga	ccgccagcgg	ggccctcacc	1080
gcagctggag	agatgaagtg	cggactatgg	ataagctctt	cctcaacggc	agcgcctaca	1140
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tcacccccgc	aacgagcccc	ggagccaaga	ccgagtttac	ggaaacggag	accaaggtcc	1260
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tcgtatgcga	atatttttta	taacatatat	ctaggatatg	tatccaagtt	caagaaggtg	2400
gactcgtagt	agaatgtggt	gatccagttg	atggccgacg	ccaactggta	tcgattacgg	2460
attggcagac	gtgccagatc	agtcggaggt	ttcttttttg	ttgggatcgc	atcacagctc	2520
caacacgaca	ttcaactttc	aa				2542

<210> 144

<211> 1542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Genomic sequence containing the coding region

<400> 144

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aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	360
tctagcatgt	tcgtttggcc	tcacaaactc	atcttgaaga	cttgtgttac	caccactctt	420
ctgtctggtc	tcacacgc	tctcgagatt	gccgctttgt	tcggtggctt	cccccaagtct	480

accgccccctt	ctcgcggaat	ctccgtcgcc	gctgcgccct	accgcgcttt	ctacagccgc	540
aagaacttcc	tggtccccga	ccgccagcgg	ggccctcacc	gcagctggag	agatgaagtg	600
cggactatgg	ataagctctt	cctcaacggc	agcgccata	tgattggcaa	gatgaatggc	660
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ggagccaaga	ccgagtttac	ggaaaacggag	accaaggtcc	tcagtgtacc	ccagggcgct	780
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gagaacgcca	agcagttcta	cctcgagaat	gccactgccg	ttgcgagaa	ccgttatcgc	900
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gcgctcggaa	ccgtgggtctc	tgaagcctgt	ggacttttct	ctgtgtatcc	taaggagaag	1080
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cggattgtcc	acgacctcga	cggctatgag	cttgtcttcc	gctattatga	acgcctggac	1500
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<210> 145

<211> 1482

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Coding region without exons

<400> 145

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gggtccagaga	aactcttgga	ggtgtggttc	gcgccttcgc	ctcaggaatt	aggtccagcg	180
cagcccgccg	gtctgaaggc	tggtccggag	gagatctgga	aggacatgtt	ggatctcgtc	240
aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	300
tctagcatgt	tcgtttggcc	tcacaaactc	atcttgaaga	cttgtggtac	caccactctt	360
ctgtctgggtc	tcccacgcat	tctcgagatt	gocgctttgt	tcggtggctt	ccccaaagtct	420
accgccccctt	ctcgcggaat	ctccgtcgcc	gctgcgccct	accgcgcttt	ctacagccgc	480
aagaacttcc	tggtccccga	ccgccagcgg	ggccctcacc	gcagctggag	agatgaagtg	540
cggactatgg	ataagctctt	cctcaacggc	agcgccata	tgattggcaa	gatgaatggc	600
gagcactggg	acttgtaact	gactgaacct	cataccatgc	tcaccccgcc	aacgagcccg	660
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gctctgcaga	ctgattcggg	ggatgagact	ttggaagtct	tgatgaccga	cttggatgag	780
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gcgctcggaa	ccgtgggtctc	tgaagcctgt	ggacttttct	ctgtgtatcc	taaggagaag	1020
tatccccgatt	cgcgcacga	tgccctacctg	tttacaccat	gcggcttctc	cgccaacggc	1080
gtgattccgc	ctcctgaggg	aaaagctgga	accactact	tcacagtaca	cgtcactcca	1140
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actctcttcg	aggccaagcc	agcgtgagc	caggtcgaag	acgagtggaa	ggaagccaag	1320
tacctggccg	ctcgtcggac	cgccaaaatg	gaacatgtgg	agggatatcg	ccgagtggac	1380
cggattgtcc	acgacctcga	cggctatgag	cttgtcttcc	gctattatga	acgcctggac	1440
tggaaagggg	gggccccctc	gctgggagag	gagagatctt	ga		1482

<210> 146

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Protein sequence

<400> 146

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1          5          10          15

Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
          20          25          30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
          35          40          45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
          50          55          60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
65          70          75          80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
          85          90          95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
          100         105         110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
          115         120         125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
          130         135         140

Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
145         150         155         160

Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
          165         170         175

Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
          180         185         190

Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
          195         200         205

Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
          210         215         220

Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
225         230         235         240

Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
          245         250         255

Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
          260         265         270

Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
          275         280         285

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His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460
 Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480
 Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 147

<211> 1637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 147

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tcattaggaa	aggtgcactc	cgtagttacc	tcgactcgcg	gttagtctgg	tgactaagtt	360
cttggcggtg	tgatgagggc	aagtcctatc	atgtgatcat	agttagggtt	tccacacacc	420
aggctctcca	atatagcaag	aaaatagaag	gattaggtct	cgtctccgaa	catccatccc	480
gccagcacac	aaccgccaaa	atgggtcgcg	ttagaaccaa	ggtaagttac	agatgaagca	540
tcatgagtta	tcttcaaaaa	agcccaaaaa	gagtatcatt	tctgacgaaa	tgggtttttc	600
ttcaatagac	agtcaagagg	tccgccaagg	tcatcatcga	gcgctactac	cccaagttga	660

cgctcgactt	tgagaccaac	aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	720
gccttcgcaa	caaggtgggc	aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	780
ctgacgaaaa	ctagattgct	ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	840
ctgtccgcgg	tatctctttc	aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtacg	900
ttcctgaggt	ttccgctctg	gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	960
ccgacacca	ggaccttctc	aagtccatgg	gcgtaagttc	tgttctcaac	gcggttggtc	1020
gtggttttaa	agcagtcctg	taacttatat	tgcccactac	agttcgacaa	tctcaaggtc	1080
aacgttgtca	acgtctccca	acatcagggt	caggagcgcc	cccgccgctt	ccggtagatg	1140
cgcgcacccc	tcgagcctcg	aaaaaaaaag	taccgattgt	cttcggtcga	tctatggcgt	1200
gctcaatcac	acttgctctg	gctgacttcg	cagctatgat	gtagcctaga	gacacaggaa	1260
tgaacataat	tctctctgag	aaaggtgtcg	ctgattctcc	tgggtggagat	gacgcttgat	1320
tgccaaaatt	tctccttttg	cttactgtcc	gtttcagctc	gggcgctgcg	tagaagggtc	1380
tctctgcatg	atgcgagga	tgtcatcaga	gagtcgaaac	ctttggtgcg	aactgcacca	1440
tcaactgcac	cgcattggat	cagatccata	ttaatcagtc	tatctacaga	agtaaattgg	1500
gtatcgatcat	aagcacaag	acgccgtaga	accacaaatc	gaaccacccc	atcgaattct	1560
gtcgtgacca	ggctcacgcc	aaaccgcgtg	agattgaagc	atatcatgat	cagatttcct	1620
ttggcacgta	gccttca					1637

<210> 148

<211> 637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Genomic sequence containing the coding region

<400> 148

atgggtcgcg	ttagaaccaa	ggtaagttac	agatgaagca	tcatgagtta	tcttcaaaaa	60
agcccaaaa	gagtatcatt	tctgacgaaa	tgggtttttc	ttcaatagac	agtcaagagg	120
tccgccaaag	tcatcatcga	gcgctactac	cccaagttga	cgctcgactt	tgagaccaac	180
aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	gccttcgcaa	caaggtgggc	240
aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	ctgacgaaaa	ctagattgct	300
ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	ctgtccgcgg	tatctctttc	360
aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtacg	ttcctgaggt	ttccgctctg	420
gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	ccgacacca	ggaccttctc	480
aagtccatgg	gcgtaagttc	tgttctcaac	gcggttggtc	gtggttttaa	agcagtcctg	540
taacttatat	tgcccactac	agttcgacaa	tctcaaggtc	aacgttgtca	acgtctccca	600
acatcagggt	caggagcgcc	cccgccgctt	ccggtag			637

<210> 149

<211> 420

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Coding region without exons

<400> 149

atgggtcgcg	ttagaaccaa	gacagtcaag	aggcccgcca	aggatcatcat	cgagcgctac	60
taccccaagt	tgacgctcga	ctttgagacc	aacaagcgtc	tttgcgatga	gatcgctatc	120
attgcctcca	agcgccttcg	caacaagatt	gctggttaca	ccaccacct	tatgaagcgt	180
atccagcgtg	gccctgtccg	cggatatctc	ttcaagctgc	aggaggagga	gcgtgagcgc	240
aaggatcagt	acgttccctga	ggtttccgct	ctggatgttt	cccagaccga	gtccggccag	300
ctcgatgtcg	atgccgacac	caaggacctt	ctcaagtcca	tgggcttcga	caatctcaag	360
gtcaacgttg	tcaacgtctc	ccaacatcag	gttcaggagc	gccccgcgcg	cttcgggtag	420

<210> 150

<211> 139
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
 Protein sequence

<400> 150

Met	Gly	Arg	Val	Arg	Thr	Lys	Thr	Val	Lys	Arg	Ser	Ala	Lys	Val	Ile
1				5					10					15	
Ile	Glu	Arg	Tyr	Tyr	Pro	Lys	Leu	Thr	Leu	Asp	Phe	Glu	Thr	Asn	Lys
			20					25					30		
Arg	Leu	Cys	Asp	Glu	Ile	Ala	Ile	Ile	Ala	Ser	Lys	Arg	Leu	Arg	Asn
		35					40					45			
Lys	Ile	Ala	Gly	Tyr	Thr	Thr	His	Leu	Met	Lys	Arg	Ile	Gln	Arg	Gly
	50					55				60					
Pro	Val	Arg	Gly	Ile	Ser	Phe	Lys	Leu	Gln	Glu	Glu	Glu	Arg	Glu	Arg
65					70				75					80	
Lys	Asp	Gln	Tyr	Val	Pro	Glu	Val	Ser	Ala	Leu	Asp	Val	Ser	Gln	Thr
			85					90					95		
Glu	Ser	Gly	Gln	Leu	Asp	Val	Asp	Ala	Asp	Thr	Lys	Asp	Leu	Leu	Lys
		100					105						110		
Ser	Met	Gly	Phe	Asp	Asn	Leu	Lys	Val	Asn	Val	Val	Asn	Val	Ser	Gln
	115					120						125			
His	Gln	Val	Gln	Glu	Arg	Pro	Arg	Arg	Phe	Arg					
	130					135									

<210> 151
 <211> 2037
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA262; clone 10-2-18
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 151

aaggtagtag	gtgcagatat	tggtgataga	catttcaaaa	tgtattagtt	acatgattac	60
ttacttagat	gtaatctttc	gataataactt	tctagtcttg	ttgagttcag	aaggccagtg	120
tgtgctgaaa	atgacagcga	cctatgcggt	gcccgtag	cgaagagcac	tggttgaaa	180
taagaagttt	attagaggag	cctcatgatg	cataatcatt	gtaagcgac	gatgcacaat	240
aatatatccg	aatttctcca	gatgacacta	agataataac	gaaaatatca	catgacgttg	300
tgggcaggta	tgtattatgt	aatctgatcg	gtagggccga	tgtctcgctt	agcggacttt	360
tctgtgggat	tgcaatttca	acttattatt	ccgccgacca	gcaacaaagc	ggttactcga	420
ctcgactccc	tccaccagag	cccgtggtgt	gatataacctg	tctgtctttg	atcctcgcaa	480
gatagacttg	agtcgcagtt	atggcggttg	gaaagtatgc	caattcactt	ctattattgt	540
tctgaacgct	tttagcatgt	gtctggatac	ggtggtttac	aggtactgat	ccgggaacag	600
gaacaagcgc	ttgtcgaagg	gcaagaaggg	tgtaagaag	aggaccgttg	atcctttctc	660
caggaaggac	gaataactctg	ttaaggatatg	tcgacgtgga	ctgtgtaagt	cgaccgcagc	720
taatctatat	caggcgcctt	ccactttcca	gatcagagag	tatgttgcac	gcatatgatg	780

tcgaattgca	ggataaaggc	gattcacaaat	ggtagtggag	attatgctga	ctgaattata	840
gtgtcgggaa	gactctggtc	aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	900
agggtcgaat	tttcgaggtc	tcgctggctg	acctgcagaa	tgatgaagac	catgctttcc	960
gcaagggttaa	gcttcgtgtg	gacgagggtc	agggaagaa	ctgtttgacc	aacttccacg	1020
gtcttgattt	cacaaccgac	aaattgcat	ccctcgtgcg	caagtggcag	tcgctgatcg	1080
aagccaatgt	cactgtgaag	acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	1140
tcaccaagag	acgcccgaac	cagattaaga	agaccacata	tgctcgttct	tctcaaatcc	1200
gtgccatccg	caagaagatg	attgaaatca	tgagaggga	ggcagccagc	tgctctctcg	1260
ctcagctcac	tcacaagctc	attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	1320
agggaaatcta	tcctttgcag	aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	1380
aactgcaatc	taggtccata	ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	1440
gggtgcactg	ctgaatctgc	acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	1500
gagagagttc	aaggagcagg	ttctcgaaag	cgtttaagt	gactgaatta	ccagtatgct	1560
ggttattcgg	gacattgatt	tgtacctacc	tgtatgcttg	gattcttttt	ttatgagtta	1620
aaatgggaaa	agaacttttg	tcgcggcatc	atgtctttat	tgactgggtg	tgctggttaac	1680
ttctatgtcc	tttgagaatg	gagcttgcaa	agaaaacttt	gcccttattc	aaatatttaa	1740
ttggacaatt	ccgatcaaag	tttagcagta	gaatacctgc	tataccagtg	atgtgctgat	1800
gcaacgggca	cctgcagttt	actttcagtt	gattcaaatt	ctatattaac	agagcccttt	1860
taccacacca	ctgacctggt	attagtatag	tgtctcgccc	taggagacta	aagaattgct	1920
agaagtatgg	ttatacataa	tgttgaatag	ttagtatgat	ttattaatat	tattttcagt	1980
gcactgatat	atatcataat	gctactaaat	atagctaccc	taagatttat	atagaga	2037

<210> 152

<211> 1037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing the coding region

<400> 152

atggcggttg	gaaagtatgc	caattcactt	ctattattgt	tctgaacgct	tttagcatgt	60
gtctggatac	ggtggtttac	aggtactgat	ccgggaacag	gaacaagcgc	ttgtcgaagg	120
gcaagaagg	tgtaagaag	aggaccgttg	atcctttctc	caggaaggac	gaataactctg	180
ttaagggtatg	tcgacgtgga	ctgtgtgaag	cgaccgcagc	taatctatat	caggcgctt	240
ccactttcca	gatcagagag	tatgttgac	gcataatgatg	tcgaattgca	ggataaaggc	300
gattcacaaat	ggtagtggag	attatgctga	ctgaattata	gtgtcgggaa	gactctggtc	360
aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	agggctcgaat	tttcgaggtc	420
tcgctggctg	acctgcagaa	tgatgaagac	catgctttcc	gcaagggttaa	gcttcgtgtg	480
gacgaggttc	agggaagaa	ctgtttgacc	aacttccacg	gtcttgattt	cacaaccgac	540
aaattgcat	ccctcgtgcg	caagtggcag	tcgctgatcg	aagccaatgt	cactgtgaag	600
acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	tcaccaagag	acgcccgaac	660
cagattaaga	agaccacata	tgctcgttct	tctcaaatcc	gtgccatccg	caagaagatg	720
attgaaatca	tgagaggga	ggcagccagc	tgctctctcg	ctcagctcac	tcacaagctc	780
attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	agggaaatcta	tcctttgcag	840
aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	aactgcaatc	taggtccata	900
ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	gggtgcactg	ctgaatctgc	960
acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	gagagagttc	aaggagcagg	1020
ttctcgaaa	cgtttaa					1037

<210> 153

<211> 771

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Coding region without exons

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<400> 153
atggcggttg gaaagaacaa gcgcttgctg aagggcaaga aggggtgttaa gaagaggacc      60
gttgatcctt tctccaggaa ggacgaatac tctgttaagg cgccttccac tttccagatc      120
agagatgtcg ggaagactct ggtcaaccgc accagtggtc tcaagaacgc caatgactcc      180
ctgaagggtc gaattttcga ggtctcgtcg gctgacctgc agaatgatga agaccatgct      240
ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc      300
cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg      360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc      420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa      480
atccgtgcca tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct      540
ctcgtcagc tcaactacaa gctcattcct gaggtcattg gtcgtgagat cgagaaggct      600
ccccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct      660
cccaagtctg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag      720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgttta a              771

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<210> 154

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18
Protein sequence

<400> 154

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
1          5          10          15

Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
20        25        30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
35        40        45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
50        55        60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65        70        75        80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
85        90        95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
100       105       110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
115       120       125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
130       135       140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
145       150       155       160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
165       170       175

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Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
 180 185 190
 Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
 195 200 205
 Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
 210 215 220
 Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
 225 230 235 240
 Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
 245 250 255

<210> 155

<211> 1819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 155

aattcatcag	cataacgaac	ccccaacgac	ttcgaaaaaa	aagcccgatt	cgaaagaatt	60
gcgcattcaa	cataccatgg	tgggcggcgt	cgtgtcgtgt	cgtacgggta	ttgtcgacaa	120
tgaggattga	agatgggcca	ggtcaatttg	ggatgttcgt	tgtgggacta	gggttttttt	180
ctgtgttggt	gcggtcacgc	tgccggctggg	ctaagcgggc	acgtgactgt	ggctgactgc	240
ctggtgacgc	cccccccgg	aggaaccccc	aaccggcagc	cagataggct	cgaggagatc	300
atcgctgaat	gatggcattg	ttcttggctt	cagtggatgg	gttattaatg	actgcctgga	360
cggctggatg	actccgtcgc	tgatttagca	ttgtgatcca	cgatttatgt	ttcattttctg	420
gggcgcgggt	ttactaccat	cacttttgtc	actaccatca	cttttatact	gagttttctga	480
ccccgacccc	gaaccagact	atggcaactt	cgactgggac	cggatgggct	cagctccggc	540
agcaagcccg	ttcgcttgag	actcaggtag	ggaactcgaa	actacgctat	aatgaggcct	600
tactcgtgat	ttggatgttg	acaataatgt	tcctagaccg	agagtctgtt	tcacacctat	660
gcgcagtatg	catcgatgac	gaagctgcct	ccgaaaccct	cagaagaaga	acaacggatt	720
gaatcgcaac	tgaaggatct	tcttgaaaag	gtgtgcactt	tgaggccctc	tagtccagcc	780
caacagacga	tcatgctgac	acgatccgat	catagcgtga	agccctcatc	tcccagctct	840
cccgtctcct	tgactccgaa	gccactctta	ccgcactctgc	cctgaaacag	agcaatcttg	900
cccgcaatcg	cgaagtcctc	caggatcatc	gccgcgaatt	gcagcgcttg	aacgcgcgaa	960
tcgccgagtc	ccgcgaccga	gccaatcttc	tgtctaactg	ccgctccgac	attgatgcct	1020
accgcaattc	aaaccccggc	gcggctgagg	cagactacat	gctcgaggag	cggggtcgta	1080
tagatgaaag	ccataacatg	atagatggtg	tcctaagcca	ggcgtatgca	atcaacgaga	1140
gttttgggct	acaacgtgaa	accctggcca	gcataaatcg	ccgtatcgtc	ggtgctgcca	1200
ataaggtacc	aggaatgaat	gcattgattg	gtaagattgg	gacgaagagg	agacgtgacg	1260
caatcatctt	gggggctttc	atcggtcttt	gtttcttgat	ggtgttcttc	ttccgatgag	1320
atgctggtgc	tccgtatacc	gccgatcttc	ctgtgttata	attccttgct	caacggtatc	1380
tacatcgag	accgcacggc	gttcgggtgt	tttcatgtac	tccttttctg	catgcaagca	1440
ctaatacaca	tggtcatggc	gtttcagggt	gtctatttca	catttatgta	catacagggt	1500
cagactgctg	tagccctagg	gctcaccgca	tgatcactct	tggttttcgga	cttgccgatt	1560
caccttggtt	tcttcccggc	cattcctcag	ccggtagctt	cgactcgaga	ctgattcttc	1620
tctcctggat	taattttgcga	accccgttgt	tcaatccgtc	tagctcgctt	tcctctgccg	1680
gcccgctacc	cgcccatcgg	atgcgacagt	tctcgtccag	cagatagaca	taaccaactt	1740
tactgttcat	cattccgatt	gcttctttca	acccatccgt	aagacctttg	cgcacaagga	1800
aataccgttc	gtgctgctc					1819

<210> 156

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Genomic sequence containing the coding region

<400> 156

atggcaactt	cgactgggac	cggatgggct	cagctccggc	agcaagcccg	ttcgcttgag	60
actcaggtac	ggaactcgaa	actacgctat	aatgaggctt	tactcgtgat	ttggatgttg	120
acaataatgt	tcctagaccg	agagtctgtt	tcacacctat	gcgcagtatg	catcgatgac	180
gaagctgcct	ccgaaaccct	cagaagaaga	acaacggatt	gaatcgcaac	tgaaggatct	240
tcttgaaaag	gtgtgcaact	tgaggccctc	tagtccagcc	caacagacga	tcattgctgac	300
acgatccgat	catagcgtga	agccctcatc	tcccagctct	cccgtctcct	tgactccgaa	360
gccactctta	ccgcatctgc	cctgaaacag	agcaatcttg	cccgcaatcg	cgaagtcctc	420
caggatcatc	gccgcgaatt	gcagcgcctg	aacgcccga	tcgccgagtc	ccgcgaccga	480
gccaatcttc	tgtctaactg	ccgctccgac	attgatgcct	accgcaattc	aaaccccgcc	540
gcggctgagg	cagactacat	gctcgaggag	cggggtcgta	tagatgaaag	ccataacatg	600
atagatgggtg	tcctaagcca	ggcgtatgca	atcaacgaga	gttttgggct	acaacgtgaa	660
accctggcca	gcatcaatcg	ccgtatcgtc	ggtgctgcca	ataaggtacc	aggaatgaat	720
gcattgattg	gtaagattgg	gacgaagagg	agacgtgacg	caatcatctt	gggggctttc	780
atcggctttt	gtttcttgat	ggtgttcttc	ttccgatga			819

<210> 157

<211> 684

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Coding region without exons

<400> 157

atggcaactt	cgactgggac	cggatgggct	cagctccggc	agcaagcccg	ttcgcttgag	60
actcagaccg	agagtctgtt	tcacacctat	gcgcagtatg	catcgatgac	gaagctgcct	120
ccgaaaccct	cagaagaaga	acaacggatt	gaatcgcaac	tgaaggatct	tcttgaaaag	180
cgtgaagccc	tcattctccc	gctctcccg	ctccttgact	ccgaagccac	tcttaccgca	240
tctgccctga	aacagagcaa	tcttgcccgc	aatcgcgaa	tcctccagga	tcattcgccgc	300
gaattgcagc	gcctgaacgc	cgcaatcgcc	gagtcgccgc	accgagccaa	tcttctgtct	360
aacgtccgct	ccgacattga	tgcctaccgc	aattcaaacc	ccgccgcggc	tgaggcagac	420
tacatgctcg	aggagcgggg	tcgtatagat	gaaagccata	acatgataga	tggtgtccta	480
agccaggcgt	atgcaatcaa	cgagagtgtt	gggctacaac	gtgaaaccct	ggccagcatc	540
aatcgccgta	tcgtcggtgc	tgccaataag	gtaccaggaa	tgaatgcatt	gattggtaag	600
attgggacga	agaggagacg	tgacgcaatc	atcttggggg	ctttcatcgc	cttttgtttc	660
ttgatgggtg	tcttcttccg	atga				684

<210> 158

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Protein sequence

<400> 158

Met	Ala	Thr	Ser	Thr	Gly	Thr	Gly	Trp	Ala	Gln	Leu	Arg	Gln	Gln	Ala
1					5			10						15	

Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
 20 25 30
 Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
 35 40 45
 Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
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 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
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<210> 159

<211> 2601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 159

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<210> 160

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing the coding region

<400> 160

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<210> 161

<211> 1185

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Coding region without exons

<400> 161

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<210> 162

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Protein sequence

<400> 162

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 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met
 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
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 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
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 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
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 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe
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<210> 163

<211> 2539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 164

<211> 1539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Genomic sequence containing the coding region

<400> 164

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<210> 165

<211> 1539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Coding region without exons

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tttcttttct ccgtcggtct ctggtgggta ggagttgtcg gtaatggttt cctggttgga 1260
agcacggcgg ccaatggctg gctagtcaaa gaggcctaca aattctggcg gcaccaaggc 1320
gccaacggca gtgctcgacg cctcttcttg gccagtattt ggcagctgcc aatcctcctt 1380
gtcggtggtc tggtcacgaa gaaaggtctc tgggatggtg tctggaacaa tgttttcggt 1440
cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg 1500
gagcgcaaga tgatacctgc gaagacgagt agctcgtga 1539

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<210> 166

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Protein sequence

<400> 166

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Met Ile Tyr Leu Arg Ser Ser Leu Leu Arg Ser Gly Leu Ala Arg Asp
1           5           10           15

Pro Ala Arg Leu Cys Ser Gln Cys Phe Ser Arg Leu Ser Pro Ser Arg
          20           25           30

Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
          35           40           45

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr
          50           55           60

Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala
          65           70           75           80

Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly
          85           90           95

Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu
          100          105          110

Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn
          115          120          125

Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr
          130          135          140

Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala

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145		150		155		160									
Phe	Leu	Ala	Leu	Thr	Lys	Pro	Arg	Leu	Ser	Phe	Leu	Ile	Val	Leu	Thr
				165					170					175	
Thr	Thr	Ser	Ala	Tyr	Gly	Met	Tyr	Pro	Ile	Ser	Ser	Leu	Leu	Thr	Leu
			180					185					190		
Asp	Pro	Ser	Met	Thr	Pro	Leu	Pro	Thr	Leu	Ser	Thr	Ser	Thr	Leu	Thr
		195					200					205			
Phe	Leu	Tyr	Leu	Thr	Thr	Gly	Thr	Phe	Leu	Ser	Ser	Cys	Ser	Ala	Asn
	210					215					220				
Thr	Leu	Asn	Met	Leu	Leu	Glu	Pro	Lys	Tyr	Asp	Ala	Leu	Met	Ser	Arg
225					230					235					240
Thr	Arg	Asn	Arg	Pro	Leu	Val	Arg	Gly	Leu	Leu	Ser	Arg	Arg	Ala	Ala
				245					250					255	
Val	Leu	Phe	Ala	Ile	Ala	Thr	Ala	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Tyr
			260					265					270		
Ile	Gly	Thr	Asn	Pro	Thr	Thr	Thr	Ala	Leu	Ser	Ala	Ser	Asn	Ile	Cys
		275					280					285			
Leu	Tyr	Ala	Phe	Val	Tyr	Thr	Pro	Leu	Lys	Arg	Ile	Ser	Val	Ile	Asn
	290					295					300				
Thr	Trp	Val	Gly	Ala	Val	Val	Gly	Gly	Ile	Pro	Pro	Leu	Met	Gly	Trp
305					310					315					320
Thr	Ala	Ala	Ala	Gly	Gln	Thr	Ala	Thr	Thr	Gly	His	Asp	Ser	Trp	Arg
				325					330					335	
Asp	Met	Leu	Phe	Ser	Lys	Asp	Ser	Ile	Gly	Gly	Trp	Leu	Leu	Gly	Gly
			340					345					350		
Ile	Leu	Phe	Ala	Trp	Gln	Phe	Pro	His	Phe	Asn	Ala	Leu	Ser	Tyr	Met
		355					360					365			
Ile	Arg	Glu	Glu	Tyr	Lys	Ala	Ala	Gly	Tyr	Arg	Met	Leu	Ala	Trp	Thr
	370					375					380				
Asn	Pro	Ala	Ala	Asn	Ala	Arg	Val	Ala	Leu	Arg	Tyr	Ser	Leu	Leu	Met
385					390					395					400
Phe	Pro	Phe	Ser	Val	Gly	Leu	Trp	Trp	Val	Gly	Val	Val	Gly	Asn	Gly
				405					410					415	
Phe	Leu	Val	Gly	Ser	Thr	Ala	Ala	Asn	Gly	Trp	Leu	Val	Lys	Glu	Ala
			420					425					430		
Tyr	Lys	Phe	Trp	Arg	His	Gln	Gly	Ala	Asn	Gly	Ser	Ala	Arg	Arg	Leu
		435					440					445			
Phe	Trp	Ala	Ser	Ile	Trp	Gln	Leu	Pro	Ile	Leu	Leu	Val	Gly	Gly	Leu
	450					455					460				
Val	Thr	Lys	Lys	Gly	Leu	Trp	Asp	Gly	Val	Trp	Asn	Asn	Val	Phe	Gly
465					470					475					480

Gln Pro Val Glu Asp Glu Asp Asp Tyr Leu Trp Glu Asp Glu Asp Glu
485 490 495

Val Ala Glu Ala Glu Arg Lys Met Ile Pro Ala Lys Thr Ser Ser Ser
500 505 510

<210> 167

<211> 2679

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 167

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tctcgagaat	tcggtgagaa	agcaagggtac	agaagagaac	tactccgtac	tctgtactct	240
gtagagaaaag	gcaggagggt	caaacatgat	tggcccggtg	agaataagaa	aatatcatgc	300
cttaggtcca	aaggctagt	ctcacatgac	cttatcagtt	gagtcagggt	atcttatcgt	360
tgtcccagag	agatgtgaag	aattattgca	ccggggagca	cgcaaggaaa	ccattctatc	420
ctatctcgtc	cctttagatt	accacaggac	atctacatct	tgaaccttac	cattccaaat	480
tacagactgc	ctctgagtac	atgctcaacg	ccgcggttgc	tgccccgcga	tgttttgtat	540
atcccactga	tcgcgcagca	atgcgcttgg	gctttgtctt	tcgtctctcc	tctcctgcac	600
ctctcttctc	aacagcacct	ttccgtcgac	agttgcatgc	ttccggcgctc	cgatcaattg	660
aacctgttat	ctttcgaaat	agccttgaaa	agactcttga	ggctcatcga	tcctccaatc	720
gagccagctc	gatccgcaag	gtgattaaac	acgattgtcc	tgctgaaaacg	ccccctccaa	780
ttttaccact	tgagaatcgt	gctggctcatg	atcaatcatc	tcaaaaggcc	tcctccgtgt	840
caaatgcaga	gtcagagtcc	ccccggtctt	ctgcgcctgc	gagacgagcg	cagaggaagg	900
cccgttcgcc	cagccaagta	gccacccgc	agccccagac	aacagaatat	ccacaactgc	960
aatggcatgc	agatgaaacc	aagggccgac	cggcacaag	tccttggctg	aagtacttga	1020
ctaccgattg	gaaaacgccc	gatgccgttt	cgcgtctcga	cgcgagatc	cgcgctcttg	1080
agctctacat	gacaccgacc	ccgtcggagc	ggactgagat	agatcggctg	ggtgcagata	1140
tgggtaggtt	gctagcggga	atcgtcccca	gcccgcacca	ggttaaccgg	tcatggcgga	1200
cgcgatttgc	cttgagccac	tcgggtctcg	attttgtctt	acctgtcccg	gattcagacc	1260
gatccacccg	tgacgttcgc	aagccgagtg	ccacacggcc	caaggtgctc	cagacttaca	1320
aaaagctctt	acatgaagt	ggacatgcgc	ttcagcagtc	cccctcgctc	gcggagcgag	1380
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ggggtaggta	tggccgtact	cagatgtcta	ttgaatccga	tgccctcgta	atgcttctcg	1620
tggccttcct	caaaatgaac	cacgggcgtt	ttcagcggcc	cgactgtctc	ggcgagcagc	1680
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ccgatgatct	acccgcgcat	ctgcgcggcc	agcgtccctc	catcagcctc	aagagaacag	1860
cagccgccag	acgcaatctg	cctgcgcgca	gccggctgtg	cgtgcaggac	cccaccaatt	1920
acatgaatga	tctggggcgc	agctgcgtgc	gtacgttgga	actccagcac	acgttctcgc	1980
ttgctcatga	ccgtctcggc	gcaagtctca	agcgttgga	tgacagtga	ccggccgcga	2040
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ccaaatcgct	taagctcaac	gcgacctagc	aatgaaactg	gccagagcct	tggagcttgg	2160
gacattgcag	cctatcttat	ttctcaactc	cattactgat	agtaaattat	atatgagata	2220
atgtggagtc	cggcaacgtg	tttcgtcacc	tgggctaata	cctgtcactg	gccactatgt	2280
agatgcagtt	gactcaatag	agggctcgta	taatcaaaca	tcagacaatg	cacgagtaga	2340
acagatggaa	tatgcttgta	agagaacgcc	cgtcttcctag	tcaagcagct	ctgaagagca	2400
aaacaatat	tccaaaccgg	ctctattcga	acgaaaatgc	ggaaataacc	atgacagaca	2460
aagaagagac	aagccaggcc	agggcaaaaag	tagtctatga	catgaattca	acgatcaaga	2520
tcacgccggt	gtatgagaac	tccagggtta	gcaataccaa	caatcgacat	gtatggcacc	2580

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gcaaggaaaa gcaccgcgga accatacgag gatatacgat cgatcaattg ctgcccctct 2640
gtcagcagct atttccattg ctgacgggat gctgatggg 2679

```

```

<210> 168
<211> 1629
<212> DNA
<213> Aspergillus fumigatus

```

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<220>
<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
      Genomic sequence containing the coding region

```

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<400> 168
atgctcaacg ccgcggttgc tgccccgcga tgttttgtat atcccaactga tcgcgcagca 60
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ttccgtcgac agttgcatgc ttccggcgtc cgatcaattg aacctgttat ctttcgaaat 180
agccttgaaa agactcttga ggctcatcga tcctccaatc gagccagtct gatccgcaag 240
gtgattaacc acgattgtcc tgctgaaacg cccctccaa ttttaccact tgagaatcgt 300
gctggtcatg atcaatcatc tcaaaaggcc tcctccgtgt caaatgcaga gtcagagtcc 360
ccccggtctt ctgcgcctgc gagacgagcg cagaggaagg cccgttcgcc cagccaagta 420
gccaccccgc agcccagac aacagaatat ccacaactgc aatggcatgc agatgaaacc 480
aagggccgac cggcacaaag tccttggtcg aagtacttga ctaccgattg gaaaacgccc 540
gatgccgttt cgcgtctcga cgcggagatc cgcgctcttg agctctacat gacaccgacc 600
ccgtcggagc ggactgagat agatcggctg gttgcagata tgggtagggt gctagcggga 660
atcgtcccca gcccgcccca ggtaaccggt tcatggcgga cgcgatttgc cttgagccac 720
tcgggtctcg attttgcctt acctgtcccg gattcagacc gatccaccgg tgacgttcgc 780
aagccgagtg ccacacggcc caaggtgctc cagacttaca aaaagctctt acatgaagtg 840
ggacatgcgc ttcagcagtc cccctcgttc gcggagcgag tccgcatcat aggagccgt 900
ttccccgtcc tctcagccat ccctgcgcc acgggcccgc tgctgcagtt cactgcggt 960
gaagggctac cggcctctgt cgaatacatc atggattacc aggccgagta tccctcgatc 1020
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cagatgtcta ttgaatccga tgccctcgta atgcttctcg tggccttctt caaaatgaac 1140
cacgggcgtt ttcagcggcc cgactgtctc ggcgagcagc tgatcgcgtt tctgcgcgcc 1200
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aatgctagta cggtcaaacg cgccagcgcc ctgtacgcgc ccgatgatct acccgcgcat 1320
ctgcgcggcc agcgtccct catcagcctc aagagaacag cagccgccag acgcaatctg 1380
cctgccgcca gccggctgtg cgtgcaggac cccaccaatt acatgaatga tctgggccgc 1440
agctgcgtgc gtacgttga actccagcac acgttctcgc ttgctcatga ccgtctcggc 1500
gcaagtctca agcgttgga tgacagtga ccggccgcga acgttagtat cctgacacgg 1560
gccctgcaag caaacttttc tgattttgaa aatctacgcg ccaaactcgt taagctcaac 1620
gcgacctag 1629

```

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<210> 169
<211> 1629
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
      Coding region without exons

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<400> 169
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atgcgcttgg gcttttgcctc tcgtctctcc tctcctgcac ctctcttctc aacagcacct 120
ttccgtcgac agttgcatgc ttccggcgtc cgatcaattg aacctgttat ctttcgaaat 180
agccttgaaa agactcttga ggctcatcga tcctccaatc gagccagtct gatccgcaag 240
gtgattaacc acgattgtcc tgctgaaacg cccctccaa ttttaccact tgagaatcgt 300
gctggtcatg atcaatcatc tcaaaaggcc tcctccgtgt caaatgcaga gtcagagtcc 360
ccccggtctt ctgcgcctgc gagacgagcg cagaggaagg cccgttcgcc cagccaagta 420

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gccaccccg c agccccagac aacagaatat ccacaactgc aatggcatgc agatgaaacc 480
aagggccgac cggcacaaag tccttggctg aagtacttga ctaccgattg gaaaacgccc 540
gatgccgttt cgcgtctcga cgcggagatc cgcgctcttg agctctacat gacaccgacc 600
ccgtcggagc ggactgagat agatcggctg gttgcagata tgggtagggt gctagcggga 660
atcgtcccca gcccgcccca ggtaaccggt tcatggcgga cgcgatttgc cttgagccac 720
tcgggtctcg attttgtctt acctgtcccg gattcagacc gatccacccg tgacgttcgc 780
aagccgagtg ccacacggcc caaggtgctc cagacttaca aaaagctctt acatgaagtg 840
ggacatgcgc ttcagcagtc cccctcgttc gcggagcgag tccgcatcat aggcagccgt 900
ttccccgtcc tctcagccat ccatcgcccc acgggcccgc tgctgcagtt cactgcggt 960
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cagatgtcta ttgaatccga tgccctcgta atgcttctcg tggccttcct caaaatgaac 1140
cacgggcgtt ttcagcgcc cgactgtctc ggcgagcagc tgatcgctt tctgcgcgcc 1200
tacggcagcg atattgacct gaccaccacc ggtgtgtccg tcgatcccc cagttggttc 1260
aatgctagta cggcctcaacg cgccagcgcc ctgtacgcgc ccgatgatct acccgcgcat 1320
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gcaagtctca agcgtggga tgacagtga cgggccgcga acgttagtat cctgacacgg 1560
gccctgcaag caaacttttc tgattttgaa aatctacgcg ccaaatcgct taagctcaac 1620
gcgacctag

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<210> 170

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Protein sequence

<400> 170

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Met Leu Asn Ala Ala Val Ala Ala Pro Arg Cys Phe Val Tyr Pro Thr
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Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro
          20           25           30

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```

Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
          35           40           45

```

```

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
          50           55           60

```

```

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
          65           70           75           80

```

```

Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
          85           90           95

```

```

Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser
          100          105          110

```

```

Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg
          115          120          125

```

```

Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
          130          135          140

```

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Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr

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145		150		155		160
Lys Gly Arg Pro	Ala Gln Ser Pro Trp	Leu Lys Tyr Leu Thr Thr	Asp			
	165	170	175			
Trp Lys Thr Pro	Asp Ala Val Ser Arg	Leu Asp Ala Glu Ile Arg	Ala			
	180	185	190			
Leu Glu Leu Tyr Met Thr	Pro Thr Pro Ser Glu Arg Thr	Glu Ile Asp				
	195	200	205			
Arg Leu Val Ala Asp Met	Gly Arg Leu Leu Ala Gly Ile Val Pro Ser					
	210	215	220			
Pro Pro Gln Val Thr	Gly Ser Trp Arg Thr Arg Phe Ala Leu Ser His					
	225	230	235			240
Ser Gly Leu Asp Phe Val Leu Pro Val	Pro Asp Ser Asp Arg Ser Thr					
	245	250	255			
Arg Asp Val Arg Lys Pro Ser Ala Thr Arg Pro Lys Val Leu Gln Thr						
	260	265	270			
Tyr Lys Lys Leu Leu His Glu Val Gly His Ala Leu Gln Gln Ser Pro						
	275	280	285			
Ser Phe Ala Glu Arg Val Arg Ile Ile Gly Ser Arg Phe Pro Val Leu						
	290	295	300			
Ser Ala Ile His Arg Pro Thr Gly Arg Leu Leu Gln Phe His Cys Gly						
	305	310	315			320
Glu Gly Leu Pro Ala Ser Val Glu Tyr Ile Met Asp Tyr Gln Ala Glu						
	325	330	335			
Tyr Pro Ser Ile Arg Pro Leu Tyr Val Thr Ala Arg Leu Ile Leu Glu						
	340	345	350			
Ala Arg Gly Arg Tyr Gly Arg Thr Gln Met Ser Ile Glu Ser Asp Ala						
	355	360	365			
Leu Val Met Leu Leu Val Ala Phe Leu Lys Met Asn His Gly Arg Phe						
	370	375	380			
Gln Arg Pro Asp Cys Leu Gly Glu Gln Leu Ile Ala Phe Leu Arg Ala						
	385	390	395			400
Tyr Gly Ser Asp Ile Asp Leu Thr Thr Thr Gly Val Ser Val Asp Pro						
	405	410	415			
Pro Ser Trp Phe Asn Ala Ser Thr Val Lys Arg Ala Ser Ala Leu Tyr						
	420	425	430			
Ala Pro Asp Asp Leu Pro Ala His Leu Arg Gly Gln Arg Ser Leu Ile						
	435	440	445			
Ser Leu Lys Arg Thr Ala Ala Ala Arg Arg Asn Leu Pro Ala Ala Ser						
	450	455	460			
Arg Leu Cys Val Gln Asp Pro Thr Asn Tyr Met Asn Asp Leu Gly Arg						
	465	470	475			480

Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His
485 490 495

Asp Arg Leu Gly Ala Ser Leu Lys Arg Trp Asp Asp Ser Glu Pro Ala
500 505 510

Ala Asn Val Ser Ile Leu Thr Arg Ala Leu Gln Ala Asn Phe Ser Asp
515 520 525

Phe Glu Asn Leu Arg Ala Lys Ser Leu Lys Leu Asn Ala Thr
530 535 540

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<210> 171
<211> 1573
<212> DNA
<213> Aspergillus fumigatus
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<220>
<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
      Genomic sequence containing 3' and 5'-ends and the coding region
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<220>
<223> misc_feature
<223> (683)..(683)
<223> n is a, c, g, or t
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<400> 171							
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cagctagctt	cacttgagat	atcacaaagt	gctttggtcg	gcctgccacg	aggtcttgtc		180
ccatgtcaac	cacgaggatt	cagtcctctg	ctcatctcag	tccaggcag	gtttctttgc		240
tggatcttgc	ggctgatgac	cctcgcgatg	tgggtgccct	gtccgcaag	gaagcgttga		300
ttttgcagct	ctacaatcaa	atccaggaac	tggaaactgga	aaaggcactt	cttgaacaag		360
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ccacgtacac	ggtcaggaga	aaggccacca	gtactgtcct	gatgactgat	ccaacattaa		600
aagctgtttca	cttgaaagct	atatcacctg	ttgaaagggt	ttacctctt	tcagtttatg		660
cgagcatttc	aattctgcat	tcnctatac	taacgcttca	tagagctctt	ctacccctgg		720
tcaaccggcg	tgatgtgttg	tctttggcac	atgagaacct	aatgaatgcg	cacaacgcga		780
ctttgagggg	actatccaat	ttagaagtac	aaaatctaga	gctacaccag	aggaatcaag		840
agctagcgcg	gcagcttctt	gagtcgcgca	aggatgatga	ttcatggaga	gaagcactgg		900
atgatgacga	cctcaaggca	caacttgagc	agctagaggc	cgatcgcaaa	aagagcaaatt		960
caagatggga	agtcatgaaa	agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaaact		1020
gggctgaaga	cgatgagctt	acagctctag	tcatttatga	atctgatgat	taataatactg		1080
cctcgaaatt	aatgattttcg	aacaatttgg	tagtattgac	ttctccgacc	ggcgactactac		1140
aggatatgac	ttccattttat	gactagtaga	gtaaaacctca	ttcattattt	ccaactaggg		1200
cggtatatac	acagtatcgt	cttgggtcgaa	tcagcagaac	ggctgaggaa	gctcggttag		1260
gtaccgtaag	tgtcgcccag	actgccgata	acctgaagac	gcgccagcgc	ccactagaac		1320
aatcttcagt	ggccgtgaga	cccacgtgac	atcatcgtcc	atccacacta	acaagacttg		1380
actgtcagac	catatgatth	ctgctgggtg	tcccaaataa	taatcttcat	acatacattg		1440
gccctgaagc	cctggaatca	tggagaaaat	tcgaatacac	atggaaggca	attagaacct		1500
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<210>	172
<211>	573
<212>	DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
Genomic sequence containing the coding region

<220>

<223> misc_feature

<223> (183)..(183)

<223> n is a, c, g, or t

<400> 172

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atatcacctg	ttgaaagggt	ttacctcctt	tcagtttatg	cgagcatttc	aattctgcat	180
tcncctatac	taacgcttca	tagagctctt	ctaccctgg	tcaaccggcg	tgatgtgttg	240
tctttggcac	atgagaacct	aatgaatgcg	cacaacgcga	ctttgaggga	actatccaat	300
ttagaagtac	aaaatctaga	gctacaccag	aggaatcaag	agctagcgcg	gcagcttctt	360
gagtccgcga	aggatgatga	ttcatggaga	gaagcactgg	atgatgacga	cctcaaggca	420
caacttgagc	agctagaggc	cgatcgcaaa	aagagcaaat	caagatggga	agtcatgaaa	480
agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaact	gggctgaaga	cgatgagctt	540
acagctctag	tcattgatga	atctgatgat	taa			573

<210> 173

<211> 573

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
Coding region without exons

<220>

<223> misc_feature

<223> (183)..(183)

<223> n is a, c, g, or t

<400> 173

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atatcacctg	ttgaaagggt	ttacctcctt	tcagtttatg	cgagcatttc	aattctgcat	180
tcncctatac	taacgcttca	tagagctctt	ctaccctgg	tcaaccggcg	tgatgtgttg	240
tctttggcac	atgagaacct	aatgaatgcg	cacaacgcga	ctttgaggga	actatccaat	300
ttagaagtac	aaaatctaga	gctacaccag	aggaatcaag	agctagcgcg	gcagcttctt	360
gagtccgcga	aggatgatga	ttcatggaga	gaagcactgg	atgatgacga	cctcaaggca	420
caacttgagc	agctagaggc	cgatcgcaaa	aagagcaaat	caagatggga	agtcatgaaa	480
agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaact	gggctgaaga	cgatgagctt	540
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<210> 174

<211> 190

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
Protein sequence

<400> 174

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 Thr Val Arg Arg Lys Ala Thr Ser Thr Val Leu Met Thr Asp Pro Thr
 20 25 30
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 35 40 45
 Leu Leu Ser Val Tyr Ala Ser Ile Ser Ile Leu His Ser Pro Ile Leu
 50 55 60
 Thr Leu His Arg Ala Leu Leu Pro Leu Val Asn Arg Arg Asp Val Leu
 65 70 75 80
 Ser Leu Ala His Glu Asn Leu Met Asn Ala His Asn Ala Thr Leu Arg
 85 90 95
 Glu Leu Ser Asn Leu Glu Val Gln Asn Leu Glu Leu His Gln Arg Asn
 100 105 110
 Gln Glu Leu Ala Arg Gln Leu Leu Glu Ser Ala Lys Asp Asp Asp Ser
 115 120 125
 Trp Arg Glu Ala Leu Asp Asp Asp Asp Leu Lys Ala Gln Leu Glu Gln
 130 135 140
 Leu Glu Ala Asp Arg Lys Lys Ser Lys Ser Arg Trp Glu Val Met Lys
 145 150 155 160
 Ser Val Ala Ser Ala Ile Val Val Gly Ser Gly Val Asn Trp Ala Glu
 165 170 175
 Asp Asp Glu Leu Thr Ala Leu Val Ile Asp Glu Ser Asp Asp
 180 185 190

<210> 175

<211> 2593

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 175

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gcttcgactg	gaaattcgga	gatcgccata	tatttgagtt	atgtaagcac	cgccgcaggc	180
gtctcattgg	gctggggaag	ctatcaacaa	ccaccagag	cttcttgaac	ttaactccgg	240
gggtgcatga	ctaatagttt	caataatgga	cgtcggatgc	tttgtaaatac	aacggcggtc	300
ctacaatggg	gatctatgca	cagttcggtta	cataggtaaa	gttgagggca	ccaccggcga	360
gtggctcgga	gtggaatggg	atgaccccac	gcgggggaag	cattctggag	aacacaacgg	420
agtggagatat	ttacatgta	tgaaagtatt	ttcaagactg	gatagagcgg	attgactgac	480
ttgaacggaa	ggtagaagga	aacaccccac	ggctggttcg	ttcgtgcgcc	cttcgcgcagc	540
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agaagaactc	gcaagacagc	agtcaggcga	agtctctgct	gcgcgggaaa	tcatcaaatt	660
tagtagcaaaa	gtagtggaag	aggtcggctt	cgacaagatc	cggaagaaac	ttgcagagct	720
ccaggaattg	aaaatcgatc	tcctggatcg	cctatgcatc	gcaggagttc	tcctcatag	780
agcgagtcta	catgagcttg	cagaggcttg	caaggagata	gaacagacat	gtcctaagat	840

cgttgacctc	gatctgagtt	acaacttact	ggaaagctgg	gttgacattg	caaacatatg	900
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gaagcatgct	gacagttggc	agcggaaatc	gtctaggtcc	tcgacaggag	ggtctgatat	1020
tcgacgggat	cacaacacta	cacttggacg	agactctact	cgaatgggac	gaggtatgct	1080
gcacaaagct	actgcttggg	taccagttag	ctgactgact	cttgggtccc	tttagatttc	1140
agctttgaca	tatcaattcc	cgctactctc	tgctctgtct	gcctccgcaa	atcagattac	1200
ccagatcttg	acacctatca	cggataccat	cacgaccttg	acactggaaa	acaatgacat	1260
ctcttcgcta	tcctcattag	catgtctgac	ctctttgagc	aagctcgagc	acctctcgct	1320
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<210> 176

<211> 1974

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
 Genomic sequence containing the coding region

<400> 176

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gtattttcaa	gactggatag	agcggattga	ctgacttgaa	cggaaaggtag	aaggaaacac	240
cccacggctg	gttcgttcgt	gcgccttctg	cgacggaccg	acagacctcg	aggcttcctt	300
gaggcagtg	gtcacaagta	tgcttctgag	ttccaagaag	aactcgcaag	acagcagtc	360
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aagttcatca	gaagagaggt	tgagctcctg	gattcaacgc	gagacatagg	cttttggttc	1920
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<210> 177

<211> 1830

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Coding region without exons

<400> 177

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cccacgcggg	ggaagcattc	tgagagaacac	aacggagtga	gatattttac	atgtagaagg	180
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aagacattga	agctgatgtt	ggtcattcag	tacatctgtg	agaagcatgc	tgacagttgg	660
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tctcttcagt	tttccgaaaa	tctcagatcg	gtggacctat	ccagaaacaa	tatcgattct	1020
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ccttaccagt	gccgactagt	ctgggagacc	aacgagttag	accctattca	tcaggagaaa	1620
aaggacgatg	gagacgattg	ggatagtgat	gaggatgaag	ccacagctat	tgatttgagg	1680
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<210> 178

<211> 609

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Protein sequence

<400> 178

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Trp Leu Gly Val Glu Trp Asp Asp Pro Thr Arg Gly Lys His Ser Gly
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Glu His Asn Gly Val Arg Tyr Phe Thr Cys Arg Arg Lys His Pro Thr
          50          55          60

Ala Gly Ser Phe Val Arg Pro Ser Arg Arg Thr Asp Arg Pro Arg Gly
65          70          75          80

Phe Leu Glu Ala Val Arg His Lys Tyr Ala Ser Glu Phe Gln Glu Glu
          85          90          95

Leu Ala Arg Gln Gln Ser Gly Glu Val Ser Ala Ala Arg Glu Ile Ile
          100          105          110

Lys Phe Ser Ser Lys Val Val Glu Glu Val Gly Phe Asp Lys Ile Arg
          115          120          125

Lys Lys Leu Ala Glu Leu Gln Glu Leu Lys Ile Val Leu Leu Asp Arg
          130          135          140

Leu Cys Ile Ala Gly Val Leu Pro His Arg Ala Ser Leu His Glu Leu
145          150          155          160

Ala Glu Ala Cys Lys Glu Ile Glu Gln Thr Cys Pro Lys Ile Val Asp
          165          170          175

Leu Asp Leu Ser Tyr Asn Leu Leu Glu Ser Trp Val Asp Ile Ala Asn
          180          185          190

Ile Cys Gln Gln Leu Lys Arg Leu Lys Thr Leu Lys Leu Met Leu Val
          195          200          205

Ile Gln Tyr Ile Cys Glu Lys His Ala Asp Ser Trp Gln Arg Lys Ser
          210          215          220

Ser Arg Ser Ser Thr Gly Gly Ser Asp Ile Arg Arg Tyr His Asn Thr
225          230          235          240

Thr Leu Gly Arg Asp Ser Thr Arg Met Gly Arg Gly Met Leu His Lys
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Ala Thr Ala Trp Leu Pro Ile Thr Gln Ile Leu Thr Pro Ile Thr Asp
          260          265          270

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Thr Ile Thr Thr Leu Thr Leu Glu Asn Asn Asp Ile Ser Ser Leu Ser
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 305 310 315 320
 Ser Leu Gln Phe Ser Glu Asn Leu Arg Ser Val Asp Leu Ser Arg Asn
 325 330 335
 Asn Ile Asp Ser Trp Leu Phe Val Asn Glu Leu Gln Arg Val Phe Pro
 340 345 350
 Gly Leu Gln Ser Leu Arg Ile Ser Gly Asn Pro Leu Tyr Asp Lys Pro
 355 360 365
 Val Ala Pro Ser Asn Val Thr Asn Leu Pro Glu Lys Pro Met Thr Val
 370 375 380
 Asp Glu Ala Tyr Met Leu Thr Leu Ser Arg Leu Ala Ser Ile Gln Thr
 385 390 395 400
 Leu Asn Tyr Ser Lys Ile Thr Ser Gln Asp Arg Ser Asn Gly Glu Leu
 405 410 415
 Tyr Tyr Leu Ser Leu Ile Gly Lys Glu Leu Ser Ala Tyr Pro Glu Ser
 420 425 430
 Ala Glu Arg Glu Ile Leu Ala Thr His Pro Arg Tyr Gln Glu Leu Cys
 435 440 445
 Glu Lys Tyr Gly Ala Pro Thr Ile Arg Arg Ala Glu Leu Ala Gly Ala
 450 455 460
 Ala Val Asn Pro Arg Ser Val Ala Ala Arg Val Val Lys Leu Ala Phe
 465 470 475 480
 Cys Leu His Ser Ser Val Ser Ser Gly Ala Asn Gln Glu Gln Phe Arg
 485 490 495
 Val Gln Lys Ile Pro Arg Ser Phe Asn Thr Tyr Gln Val Lys Ala Ile
 500 505 510
 Ala Ser Arg Leu Phe Asn Leu Pro Pro Tyr Gln Cys Arg Leu Val Trp
 515 520 525
 Glu Thr Asn Glu Leu Asp Pro Ile His Gln Glu Lys Lys Asp Asp Gly
 530 535 540
 Asp Asp Trp Asp Ser Asp Glu Asp Glu Ala Thr Ala Ile Gly Leu Gly
 545 550 555 560
 Glu Ser Asn Lys Leu Thr Pro Ala Thr Glu Asp Gly Lys Phe Ile Arg
 565 570 575
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595

600

605

Asn

<210> 179

<211> 1867

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 179

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actgctgttt	taggactagg	tcggttttgg	gtggcagatt	atcacccgaa	ctgttttgtg	300
ataacagtga	tatcatttcc	ctttcatata	acaatttaac	actcagacat	cgatcatggca	360
gaataactgga	aatcagctgt	aagtgccctt	cattcagttc	cgcagacttc	ttcgtgataa	420
tctttacgtg	gggaagtccg	gcatcaactg	acagcaatat	tctagccccg	gttctggtgc	480
aaacaatgca	agatattcat	tcgggataca	cccttcgaga	aaacccagca	tgaagcgagt	540
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caggaggccg	agagattcgt	gagtcagggt	tggggctcga	ggactcggca	gtatcctggg	1020
gagcagagcg	atgcagacct	ggatgcactt	ctaaattcta	ccaaggatgt	aaagaaggtc	1080
aagttgtcgg	cgccggatga	agggtcgaaa	gagaaggcta	gcaaagaggg	tgctacacca	1140
agcaacgata	cggaccaggc	tgcggtcag	gagtcagaa	taccatcagt	caagtctgag	1200
ggtaaagaag	cggcgagct	tgctacaaca	gataccccag	cggatgaagca	ggaagaggag	1260
gcggcaccta	caggagttgt	ttttaagaag	cgcaagccga	aggtcctgag	gaaatagtcg	1320
aatttgcagc	tgctggatat	ctattatcta	ccatgcgcac	aaatgtacag	atgatgcgtt	1380
atggttgcgc	acggtccaat	atgcctcgcc	tgccggtgct	cacatgaagc	gatcatgggt	1440
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gggttgtctg	ataatattct	gccttacatt	ggcagagaga	cgttgagca	catagggtgg	1680
atggagaatg	atcagttctt	acgtatgtaa	gcatgatgtc	tagctcagaa	aagagtccca	1740
tataccatgc	gactcgttgg	cagcatccac	ctcttccttt	ggagtgcaat	ctacaatagc	1800
atgcatacga	aacaaatttc	gttgacaagg	agacccaggg	cgagaagagt	aatatagcaa	1860
gccagct						1867

<210> 180

<211> 963

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Genomic sequence containing the coding region

<400> 180

atggcagaat	actggaaatc	agctgtaagt	gcccttcatt	cagttccgca	gactttcttcg	60
tgataatctt	tacgtgggga	agtccggcat	caactgacag	caatattcta	gccccgggtc	120

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tgggtgcaaac aatgcaagat attcattcgg gatacacccct tcgagaaaaac ccagcatgaa 180
gcgagtgccaa aacaccaggga aaaccttaag cgttttcctac gagatatcca ccgggaaaaat 240
gaacgggaagc aaagagaaaac tcagaaggcg aaggatgaag tcgagcgatt aaggcaaaact 300
gtcgcaggaa aaccagggtgc aaaagacagc ggcgcaacag cttggaaaca cgcctcggct 360
gcccctccac cggcagaacg acctgtgtcc ctggaagaga gaaagaagca gatagcgag 420
ctggcagaga tgggaattgc tatcccggaac gaataccgtg gtgaactcgc gctcgctggc 480
gaatggcaga cggatatccga acgagttatt cgaccagatg acgatacaga ggaaggaaag 540
cctggttagct ctatcggcgt tcggaaaacgc aagatggaag gcgatgagga ggagcaggag 600
gcgcgacagg aggccgagag attcgtgagt cagggttggg gctcgaggac tcggcagtat 660
cctggggagc agagcgatgc agacctggat gcacttctaa attctacca ggatgtaaag 720
aaggtcaagt tgtcggcgcc ggatgaaggg tcgaaagaga aggctagcaa agaggggtgct 780
acaccaagca acgatacggg ccaggctgcg gctcaggagt cagaactacc atcagtcaag 840
tctgagggta aagaagcggc gcagcttgct acaacagata cccagcggt gaagcaggaa 900
gaggaggcgg cacctacagg agttgttttt aagaagcgca agccgaaggc cctgaggaaa 960
tag 963

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<210> 181

<211> 876

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Coding region without exons

<400> 181

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cgggatacac ctttcgagaa aaccagcat gaagcgagt ccaaacacca gggaaacctt 120
aagcgtttcc tacgagatat ccaccgggaa aatgaacgga agcaaagaga aactcagaag 180
gcgaaggatg aagtcgagcg attaaggcaa actgtcgag gaaaaccagg tgcaaaagac 240
agcggcgcaa cagcttgga acacgcctcg gctgcccctc caccggcaga acgacctgtg 300
tccctggaag agagaaaagaa gcagatagcg cagctggcag agatgggaat tgctatcccg 360
gacgaatacc gtggtgaact cgcgctcgct ggogaatggc agacggtatc cgaacgagtt 420
attcgaccag atgacgatac agaggaagga aagcctggta gctctatcgg cgttcggaaa 480
cgcaagatgg aaggcgatga ggaggagcag gaggcgcgac aggaggccga gagattcgtg 540
agtcagggtt ggggctcgag gactcggcag tctcctgggg agcagagcga tgcagacctg 600
gatgcacttc taaattctac caaggatgta aagaaggta agttgtcggc gccggatgaa 660
gggtcgaaaag agaaggctag caaagagggt gctacaccaa gcaacgatac ggaccaggct 720
gcggctcagg agtcagaact accatcagtc aagtcagag gttaaagaagc ggcgagctt 780
gtacaacagc atacccagc ggtgaagcag gaagaggagg cggcacctac aggagttgtt 840
tttaagaagc gcaagccgaa ggtcctgagg aaatag 876

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<210> 182

<211> 291

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Protein sequence

<400> 182

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Met Ala Glu Tyr Trp Lys Ser Ala Pro Arg Phe Trp Cys Lys Gln Cys
1           5           10           15

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Lys Ile Phe Ile Arg Asp Thr Pro Phe Glu Lys Thr Gln His Glu Ala
20           25           30

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Ser Ala Lys His Gln Gly Asn Leu Lys Arg Phe Leu Arg Asp Ile His
 35 40 45
 Arg Glu Asn Glu Arg Lys Gln Arg Glu Thr Gln Lys Ala Lys Asp Glu
 50 55 60
 Val Glu Arg Leu Arg Gln Thr Val Ala Gly Lys Pro Gly Ala Lys Asp
 65 70 75 80
 Ser Gly Ala Thr Ala Trp Lys His Ala Ser Ala Ala Pro Pro Pro Ala
 85 90 95
 Glu Arg Pro Val Ser Leu Glu Glu Arg Lys Lys Gln Ile Ala Gln Leu
 100 105 110
 Ala Glu Met Gly Ile Ala Ile Pro Asp Glu Tyr Arg Gly Glu Leu Ala
 115 120 125
 Leu Ala Gly Glu Trp Gln Thr Val Ser Glu Arg Val Ile Arg Pro Asp
 130 135 140
 Asp Asp Thr Glu Glu Gly Lys Pro Gly Ser Ser Ile Gly Val Arg Lys
 145 150 155 160
 Arg Lys Met Glu Gly Asp Glu Glu Glu Gln Glu Ala Arg Gln Glu Ala
 165 170 175
 Glu Arg Phe Val Ser Gln Gly Trp Gly Ser Arg Thr Arg Gln Tyr Pro
 180 185 190
 Gly Glu Gln Ser Asp Ala Asp Leu Asp Ala Leu Leu Asn Ser Thr Lys
 195 200 205
 Asp Val Lys Lys Val Lys Leu Ser Ala Pro Asp Glu Gly Ser Lys Glu
 210 215 220
 Lys Ala Ser Lys Glu Gly Ala Thr Pro Ser Asn Asp Thr Asp Gln Ala
 225 230 235 240
 Ala Ala Gln Glu Ser Glu Leu Pro Ser Val Lys Ser Glu Gly Lys Glu
 245 250 255
 Ala Ala Gln Leu Ala Thr Thr Asp Thr Pro Ala Val Lys Gln Glu Glu
 260 265 270
 Glu Ala Ala Pro Thr Gly Val Val Phe Lys Lys Arg Lys Pro Lys Val
 275 280 285
 Leu Arg Lys
 290

<210> 183

<211> 2193

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 183

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aacggaggct	gttaagtatt	cgccacgggg	aaatagccca	aaaggaactc	gtcacagctg	120
gaatcaacac	caagtaccga	agaaacaagc	gagcagcggc	tgtttggtt	ctgcagctgc	180
acaaaaaatg	ggaacgaagt	gaatgaggtt	agatagagat	gaggatggat	caagaagcgc	240
cctccagatg	tagcaatgaa	gagatgatgt	tgcaagaaga	ggtgaaacaa	gctggcggca	300
cgggatcagg	ctaggctaga	tagggtttagc	aacgaggggtg	acatcacgtg	agaacgggca	360
tcgtgatatg	gatgacaatt	aacatcataa	acactcttcg	ttcagttgct	gtgactcctg	420
acgcgtaagg	ggatctgggg	tgaagtcaag	caatagactc	tctgacagat	ttgacttttag	480
agaaagtaaa	taacaccact	atggacatct	cgcaagaaac	cgttgataaa	atacgacggt	540
tcgcgcaaaa	gcgccaaaaa	gcggaggagt	tctacgagga	acactcggtg	aatccagcta	600
atthttgacgc	ttacaatcgc	aagttggatg	agacgttggc	agagctgcag	gctcaagtca	660
aacgtcatga	ggatgagctc	cgcaagggtac	gtcaacaagt	tgccctagaat	ataagccgac	720
tgtcacaaga	gatttcatgc	atgaattagg	aatactgaca	agaggaacag	ctacgcatga	780
ccaccacgat	cgagttcgct	caaattgggg	cagatccttg	ggcccgcatc	tcagaagtgc	840
gcagagccaa	gaaagcgtat	gattctcttc	tgcaatcggg	aacgcgactg	ccgagtcag	900
gctcgccctt	gccttcatta	cttgcggttg	acgagggcgtc	tcgtctcgtc	aaggagagca	960
agacctcaat	ctcactgacg	gcgagagaaac	tgtctgcgga	tcgtcagcgc	ttgaaagcgg	1020
aagaagccaa	tttgcgcgat	gcgcaactga	tcaaagacgg	ggttgagaaa	aggattgagc	1080
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aacagcggat	tgacgagctt	gttcgtcgcc	aaactgcgca	ggagggcaac	gagcaggcaa	1440
cccttttgaa	caaaagagag	gcggccgcgc	ctgaaatgcg	agctcttctt	actgctctgt	1500
tagatgcgga	ttactcctat	gtcgaccttc	cgcacgagtc	agcggcctcg	cgctttctag	1560
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catcaaaagc	ttatcagaaa	gttcaatgct	cgaggtcaaa	aatataccgt	taatgccata	1920
caagaaacat	ggaagaagaa	agaccgtagc	cggttatcag	atcggcatca	ttccgatgct	1980
ggtagaagta	ctcttgcccg	tattctttgc	tttgagacca	gttcgggaac	ccgccgagcg	2040
cttggtgact	tgatcgctgg	gctcccttct	aggtcgcggc	gtttttattt	ttgaactcga	2100
ccctgtagcg	ttcttgcggt	ggaagcgctt	cttggaacgaa	gtctttcttt	tcttggaacg	2160
gctagtctcg	gtgtcttcat	actcttcgga	tga			2193

<210> 184

<211> 1448

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Genomic sequence containing the coding region

<400> 184

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gaacagcagc	gcccacaaga	tgaatccagc	tggaattcaca	ttcgcgctgt	aatttctagc	360
caggaagctg	ccacagtcac	tggcaagggt	ggagaaaacg	tatctcagat	tcgtcgtttg	420
tctggagcaa	agtgcactgt	cagcgactac	tcccgtggtg	cagtcgaacg	tattttgacc	480
gtgagcggcc	cacaggatgc	cgttgccaag	gttggttttt	tgatctatcc	ttcgtgtgtt	540
gaaagattgc	taattcagag	taggcgtttg	gtttgatcat	ccgtacattg	aacaatgaac	600
ctcttgatgc	cccctctacc	gcccattcca	agacataccc	tctgcgtttg	ctgatcccc	660

atctccttat	tggtccatc	attggcaaag	gtggttcacg	cattcgcgaa	attcaggaag	720
cttctggtgc	ccgactgaat	gcatccgatt	cgtgccttcc	cttgtcctct	gagcggtcac	780
ttgtaattct	cggcggttgc	gattctgtcc	acatcgctac	ctactacgtc	gccgtaaccc	840
tcgttgagca	gctcactgag	cgctttggag	gtcctgcagc	ctcagcttat	gccactcgca	900
gcggtggccc	tgctggagca	gtgcctggcg	gtatgcaggt	tgtcccgtat	gttccacagc	960
ccgctgggtg	tcaatatggc	catccagaac	atctcaagag	acaccatcac	caccccaatc	1020
gcgctgctgc	aggcgccctat	ggggtccctt	accttcacgg	tcagcctgct	cccgaccag	1080
tggtccagcc	ggctttgcat	tatggagctg	ctccccatgc	cccttacgca	ggagctggcc	1140
cccatcagcc	tgctccatac	ggcgcaccgc	agcccgcctca	ggcacgcggc	gctcctaccc	1200
ctgccacacc	cgttggaggt	gtcatgcctg	gtcagccatt	gactcagcag	atctacatcc	1260
ccaacgacat	ggttggtgcc	atcatcgga	agggcggtgc	gaagatcaat	gagattcgac	1320
acctcagtgg	cagtgtgatc	aagattaatg	agcctcaaga	gaacagcaat	gagcgtttgg	1380
tgactattac	tggaaaccag	gaatgcaacc	aaatggctct	gtacatgctt	tactcgcgac	1440
ttgggttag						1448

<210> 185

<211> 1395

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663

Coding region without exons

<400> 185

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ggaaacgagt	cggagaccta	tacggatgcc	aaggctgagc	cttccgctgc	gccaagtgtc	180
actgctgatg	gccagggcga	cactgttggt	cctgatgctc	caaattgtaa	gggtgcattc	240
acggagacgc	agccaattca	gtcgaccgcg	tctcatggcg	agcgcgctac	ttctcagccc	300
gaaacagcag	gccacaaga	tgaatccagc	tggattcaca	ttcgcgctgt	aatttctagc	360
caggaaagctg	ccacagtcac	tggcaagggt	ggagaaaacg	tatctcagat	tcgtcgtttg	420
tctggagcaa	agtgcactgt	cagcgactac	tcccgtgggtg	cagtcgaacg	tattttgacc	480
gtgagcggcc	cacaggatgc	cgttgccaag	gcgtttgggt	tgatcatccg	tacattgaac	540
aatgaacctc	ttgatgcccc	ctctaccgcc	caatccaaga	cataccctct	gcgtttgctg	600
atcccccatc	tccttatttg	ctccatcatt	ggcaaagggtg	gttcacgcat	tcgcgaaatt	660
caggaaagctt	ctggtgcccc	actgaatgca	tccgattcgt	gccttccctt	gtcctctgag	720
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gtaaccctcg	ttgagcagct	cactgagcgc	tttggagggtc	ctgcagcctc	agcttatgcc	840
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ccacagcccc	ctggtggtca	atatggccat	ccagaacatt	tcaagagaca	ccatcaccac	960
cccaatcgcg	ctgctgcagg	cgcttatggg	gtcccttacc	ttcacgggtc	gcctgctccc	1020
gcaccagtgg	cccagccggc	tttgcatatt	ggagctgctc	cccatgcccc	ttacgcagga	1080
gctggccccc	atcagcctgc	tccatacggc	gcaccgcagc	ccgctcaggc	acgcggcgct	1140
cctaccccctg	ccacacccgt	tggaggtgtc	atgcctgggtc	agccattgac	tcagcagatc	1200
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attcgacacc	tcagtggcag	tgtgatcaag	attaatgagc	ctcaagagaa	cagcaatgag	1320
cgtttggtga	ctattactgg	aacccaggaa	tgcaacccaaa	tggctctgta	catgctttac	1380
tcgcgacttg	gttag					1395

<210> 186

<211> 464

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663

Protein sequence

<400> 186

Met Ser Ala Ser Pro Ser Ala Leu Gln Ser Thr Lys Arg Pro Leu Glu
 1 5 10 15
 Asp Pro Ser Ser Pro Ser Gly Pro Asn Asp Gln Pro Glu Ala Lys Arg
 20 25 30
 Pro Ala Leu Asp Lys Val Val Lys Gly Asn Glu Ser Glu Thr Tyr Thr
 35 40 45
 Asp Ala Lys Ala Glu Pro Ser Ala Ala Pro Ser Ala Thr Ala Asp Gly
 50 55 60
 Gln Gly Asp Thr Val Val Pro Asp Ala Pro Asn Gly Lys Gly Ala Ser
 65 70 75 80
 Thr Glu Thr Gln Pro Ile Gln Ser Thr Ala Ser His Gly Glu Arg Ala
 85 90 95
 Thr Ser Gln Pro Glu Gln Gln Arg Pro Gln Asp Glu Ser Ser Trp Ile
 100 105 110
 His Ile Arg Ala Val Ile Ser Ser Gln Glu Ala Ala Thr Val Ile Gly
 115 120 125
 Lys Gly Gly Glu Asn Val Ser Gln Ile Arg Arg Leu Ser Gly Ala Lys
 130 135 140
 Cys Thr Val Ser Asp Tyr Ser Arg Gly Ala Val Glu Arg Ile Leu Thr
 145 150 155 160
 Val Ser Gly Pro Gln Asp Ala Val Ala Lys Ala Phe Gly Leu Ile Ile
 165 170 175
 Arg Thr Leu Asn Asn Glu Pro Leu Asp Ala Pro Ser Thr Ala Gln Ser
 180 185 190
 Lys Thr Tyr Pro Leu Arg Leu Leu Ile Pro His Leu Leu Ile Gly Ser
 195 200 205
 Ile Ile Gly Lys Gly Gly Ser Arg Ile Arg Glu Ile Gln Glu Ala Ser
 210 215 220
 Gly Ala Arg Leu Asn Ala Ser Asp Ser Cys Leu Pro Leu Ser Ser Glu
 225 230 235 240
 Arg Ser Leu Val Ile Leu Gly Val Ala Asp Ser Val His Ile Ala Thr
 245 250 255
 Tyr Tyr Val Ala Val Thr Leu Val Glu Gln Leu Thr Glu Arg Phe Gly
 260 265 270
 Gly Pro Ala Ala Ser Ala Tyr Ala Thr Arg Ser Gly Gly Pro Ala Gly
 275 280 285
 Ala Val Pro Gly Gly Met Gln Val Val Pro Tyr Val Pro Gln Pro Ala
 290 295 300
 Gly Gly Gln Tyr Gly His Pro Glu His Phe Lys Arg His His His His
 305 310 315 320

Pro	Asn	Arg	Ala	Ala	Ala	Gly	Ala	Tyr	Gly	Val	Pro	Tyr	Leu	His	Gly	
			325						330			335				
Gln	Pro	Ala	Pro	Ala	Pro	Val	Ala	Gln	Pro	Ala	Leu	His	Tyr	Gly	Ala	
			340						345			350				
Ala	Pro	His	Ala	Pro	Tyr	Ala	Gly	Ala	Gly	Pro	His	Gln	Pro	Ala	Pro	
			355						360			365				
Tyr	Gly	Ala	Pro	Gln	Pro	Ala	Gln	Ala	Arg	Gly	Ala	Pro	Thr	Pro	Ala	
			370						375			380				
Thr	Pro	Val	Gly	Gly	Val	Met	Pro	Gly	Gln	Pro	Leu	Thr	Gln	Gln	Ile	
385									390			395			400	
Tyr	Ile	Pro	Asn	Asp	Met	Val	Gly	Ala	Ile	Ile	Gly	Lys	Gly	Gly	Ala	
			405						410			415				
Lys	Ile	Asn	Glu	Ile	Arg	His	Leu	Ser	Gly	Ser	Val	Ile	Lys	Ile	Asn	
			420						425			430				
Glu	Pro	Gln	Glu	Asn	Ser	Asn	Glu	Arg	Leu	Val	Thr	Ile	Thr	Gly	Thr	
			435						440			445				
Gln	Glu	Cys	Asn	Gln	Met	Ala	Leu	Tyr	Met	Leu	Tyr	Ser	Arg	Leu	Gly	
450						455						460				

<210> 187

$\langle 211 \rangle$ 2121

<212> DNA

<213> Aspergillus fumigatus

 $\langle 220 \rangle$

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 187

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tgacaattaa	catcataaac	actcttcgtt	cagtttgtgt	gactcctgac	cgctaagggg	360
atctggggtg	aagtcaaagca	atgactcttc	tgacagattt	gacttttagag	aaagtaaata	420
acaccactat	ggacatctcg	caagaaaccg	ttgataaaat	acgacgtttc	gcgcaaaagc	480
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acaatcgcaa	gttggatgag	acgttggcag	agctgcaggc	tcaagtcaaa	cgtcatgagg	600
atgagctccg	caaggtacgt	caacaagttg	cctagaatat	aagccgactg	tcacaagaga	660
tttcatgcat	gaattaggaa	tactgacaag	aggaacagct	acgcatgacc	accacgatcg	720
agttcgctca	aattggggga	gataccttggg	cccgcattct	agaagtgcg	agagccaaga	780
aagcgtatga	ttctcttctg	caactcgaaa	cgcactgcc	gagtcaggc	tcgccttgc	840
cttcattact	tgcggttgac	gaggcgtctc	gtctcgtcaa	ggagagcaag	acctcaatct	900
cactgacggc	ggagaaactg	tctgcggatc	gtcagcgctt	gaaagcggaa	gaagccaatt	960
tgcgcgatgc	gcaactgata	aaagacgggt	tggagaaaag	gattgagcgg	ctgaacgcag	1020
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agcaggaaaa	gatcgagaga	cttgatacta	ccacagaaga	gctaaagtcc	tctctctata	1140
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<210> 188

<211> 1143

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Genomic sequence containing the coding region

<400> 188

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<210> 189

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Coding region without exons

<400> 189

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aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
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<210> 190

<211> 344

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Protein sequence

<400> 190

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35          40          45

Leu Gln Ala Gln Val Lys Arg His Glu Asp Glu Leu Arg Lys Phe Ala
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Gln Ile Gly Ala Asp Pro Trp Ala Arg Ile Ser Glu Val Arg Arg Ala
65          70          75          80

Lys Lys Ala Tyr Asp Ser Leu Leu Gln Ser Glu Thr Arg Leu Pro Ser
85          90          95

Pro Gly Ser Pro Leu Pro Ser Leu Leu Ala Val Asp Glu Ala Ser Arg
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Leu Val Lys Glu Ser Lys Thr Ser Ile Ser Leu Thr Ala Glu Lys Leu
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Ser Ala Asp Arg Gln Arg Leu Lys Ala Glu Glu Ala Asn Leu Arg Asp
130        135        140

Ala Gln Leu Ile Lys Asp Gly Leu Glu Lys Arg Ile Glu Arg Leu Asn
145        150        155        160

Ala Glu Lys Ser Ser Gln Val Gln Lys Thr Pro Ala Gln Leu Ala Tyr
165        170        175

Asp Leu Val Lys Glu Gln Gln Glu Lys Ile Glu Arg Leu Asp Thr Thr
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 Gly Lys Pro Lys Lys Pro Lys Thr Pro Ala Val Gly Thr Ser Asp Ser
 245 250 255
 Gly Gln Gln Arg Ile Asp Glu Leu Val Arg Arg Gln Thr Ala Gln Glu
 260 265 270
 Gly Asn Glu Gln Ala Thr Leu Leu Asn Lys Arg Glu Ala Ala Ala Ala
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 Glu Met Arg Ala Leu Leu Thr Ala Leu Leu Asp Ala Asp Tyr Ser Tyr
 290 295 300
 Val Asp Leu Pro His Glu Ser Ala Ala Ser Arg Phe Leu Val Arg Ala
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 Lys Val Ala Gln Phe His Pro Arg Asp Ala Arg Lys Leu Arg Leu Ile
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<210> 191

<211> 2000

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA283; clone 11-6-20; contig 4910 region 9638-11637
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 191

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acatactgtt	tcctaccttg	attggcgcaa	atccggcgac	aataatcaag	ggtagagtga	300
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<210> 192

<211> 4336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899

region 472441-476776

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 192

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<210> 193

<211> 3336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Genomic sequence containing the coding region

<400> 193

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<211> 3180

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Coding region without exons

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<210> 195

<211> 1059

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Protein sequence

<400> 195

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Ile Ile Ala Met Ala Val Ser Phe Gly Ile Gln Ser Trp Ile Glu Gly
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Thr Val Pro Ala Asp Leu Arg Leu Val Asp Ala Met Asn Phe Glu Thr
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Asp Glu Ala Leu Leu Thr Gly Glu Ser Leu Pro Val Gln Lys Glu Val
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 Glu Pro Ser Arg Pro Glu Asp Leu Leu Lys Asp Asn Pro Leu Leu Glu
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 Thr Phe Cys Gly Leu Ile Gly Leu Tyr Asp Pro Pro Arg Pro Glu Thr
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<210> 196

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 197

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<213> *Aspergillus fumigatus*

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<223> Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing the coding region

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<213> *Aspergillus fumigatus*

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contig 4899 region 477626-479684

Coding region without exons

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<223> Homologue GmZnf1; Phylum CEA284.2;
contig 4899 region 477626-479684
Protein sequence

<400> 199

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35          40          45
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50          55          60
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65          70          75          80
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	290					295					300				
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Ile	Asp	Val	Trp	His	Ala	Thr	Gln	Arg	Thr	Phe	Glu	Thr	Pro	Arg	Gly
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			340					345					350		